WEST Search History

DATE: Monday, March 03, 2003

| Set Name side by side | Query | Hit Count | Set Name result set |
|-----------------------|--|-----------|---------------------|
| DB = USH | PT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ | | |
| L36 | L33 and 114 | 1 | L36 |
| L35 | L33 and 113 | 1 | L35 |
| L34 | L33 and 112 | 0 | L34 |
| L33 | L32 and 117 | 3 | L33 |
| L32 | sodium-potassium adenosine triphosphorylase | 3 | L32 |
| L31 | L17 and 14 | 2 | L31 |
| DB = USF | PT; PLUR=YES; OP=ADJ | | |
| L30 | 117 and 14 | 1 | L3() |
| L29 | compound or composition or agent | 948383 | L29 |
| DB = USI | PT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ | • | |
| L28 | L4 and 120 | 1 | L28 |
| L27 | L4 and 119 | 2 | L27 |
| L26 | L4 and 118 | 0 | L26 |
| L25 | L4 and 15 | 1 | L25 |
| L24 | 15 same 14 | () | L24 |
| L23 | 119 and 110 | 1 | L23 |
| L22 | 120 and 110 | 1 | L22 |
| L21 | 120 and 110 | 1 | L21 |
| L20 | L13 with 19 | 46 | L20 |
| L19 | L12 with 19 | 5 | L19 |
| L18 | 114 with 19 | 38 | L18 |
| L17 | 115 adj L16 | 824 | L17 |
| L16 | transgenic | 26173 | L16 |
| L15 | rat or mouse or rodent | 229213 | L15 |
| L14 | L11 adj 13 | 13427 | L14 |
| L13 | L11 adj 12 | 29140 | L13 |
| L12 | L11 adj 11 | 27712 | L12 |
| L11 | method | 5683044 | L11 |
| L10 | Dahl Salt sensitive rat | 11 | L10 |
| L9 | hypertension | 35041 | L9 |
| L8 | blood pressure or life span or renal pathology | 52471 | L8 |
| L7 | 14 with 15 | () | L7 |
| L6 | L5 adj gene | 2 | L6 |



| L5 | hypertension susceptibility | 10 | L5 |
|----|-----------------------------|--------|----|
| L4 | Na,K-ATPase | 83 | L4 |
| L3 | screening | 148614 | L3 |
| L2 | identifying | 267653 | L2 |
| L1 | assaying or testing | 463978 | L1 |

END OF SEARCH HISTORY

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STIG-Biotech/ChemLib

From: Sent:

Whiteman, Brian Monday, March 03, 2003 2:41 PM STIC-Biotech/ChemLib

To:

seq search

Subject:

10/040,722 filed 1/7/02 CON of 09/653,030 9/1/00 Ruiz-Opazo

search seq id no: 3 against public DNA databases.

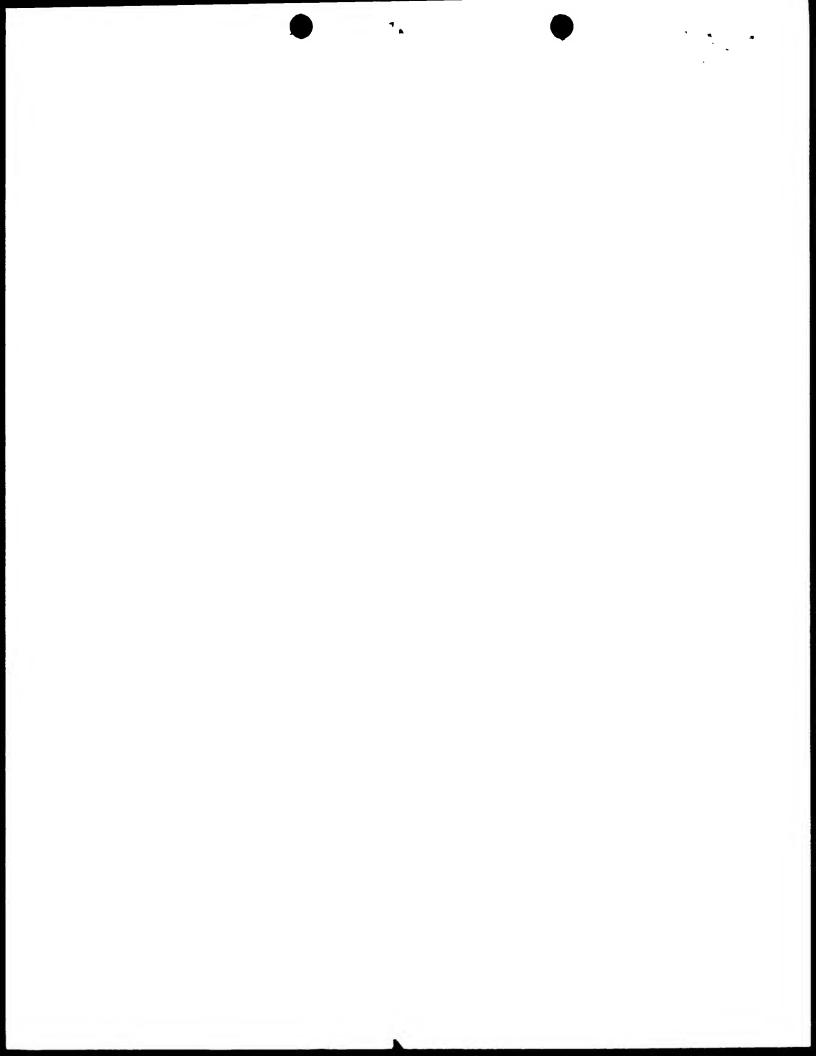
Thanks, Brian Whiteman, 11e12
Patent Examiner - Art Unit 1635
United States Patent and Trademark Office Crystal Mall 1, 11A16 (703) 305-0775

Soint or Contact Beverly Shears rechnical Info. Specialis CM1 1E05 Tel 308-4992

| Searcher: |
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| Phone: |
| Location: |
| Date Picked Up: |
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| TYPE OF SEARCH: |
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| NA Sequences: |
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| VENDOR/COST (where applic.) |
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SEARCH REQUEST FORM

| Requestor's Name: | Serial Number | :: | |
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| Date: Pl | none: | Art Unit: | |
| Search Topic: Please write a detailed statement of search topic. Desthat may have a special meaning. Give examples or rea copy of the sequence. You may include a copy of | elevant citations, authors keyw | oras, etc., ii kilowii. Poi sequeie | befine any terms es, please attach |
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| 1 3631.2 99.9 3636 6 AR175998 2 3631.2 99.9 3636 10 RATATPA1 3 3626.4 99.7 3636 6 AR175995 4 3626.4 99.7 3636 6 AR175997 5 3621.6 99.6 3636 6 AR175997 5 3621.6 99.6 3636 6 AR175997 6 3312.4 91.1 3669 10 BC025681 10 3312.4 91.1 3669 10 BC025681 11 3312.4 91.1 3669 10 BC025627 13 390.4 90.7 3599 10 RATNALPH1 13 3927.4 90.7 3599 10 RATNALPH1 14 3014.6 82.9 3297 10 BC00307 15 2856.2 78.0 4108 9 HUMNKATPA 17 2836.2 78.0 4108 9 HUMNKATPA 18 2636 73.3 3429 4 SEATPAR 19 2666 73.3 3429 4 OAATPMR 20 2471.2 68.0 3117 4 PIGATPBSEN 20 2471.2 68.0 3117 4 PIGATPBSEN 21 2436 67.3 3429 5 CHKATPAS 22 2301.6 63.3 2511 10 BC025037 23 2102.6 57.8 3355 5 CHKATPAS 23 2102.6 57.8 3392 5 XLUJ00108 26 2053.4 56.5 3392 5 XLUJ00108 26 2053.4 56.5 3399 5 XLUJ00108 27 1999.6 55.0 3397 5 XLUJ00108 28 1971.8 54.2 3390 5 TMU8254 28 1971.8 54.2 3390 5 TMU8254 29 11949 53.6 34474 5 AF286372 31 1932.6 53.2 3557 10 RNATPAHO 31 1932.6 53.2 3559 10 RNATPAHO 31 1932.6 53.2 3559 10 RNATPAHO 31 1937.4 52.7 3262 5 AV008376 31 1917.4 52.7 3262 5 AV008376 40 1916.5 52.7 5287 9 HSM803304 41 1912.4 52.6 4043 10 BC020177 |
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ALIGNMENTS

| | | Location/Qualifiers | |
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| | | Patent: US 6309874-A 8 30-OCT-2001; | JOURNAL P |
| | | Selection marker | TITLE S |
| | | Belusa, R. | AUTHORS B |
| | | 1 (bases 1 to 3636) | REFERENCE 1 |
| | | Unclassified. | u |
| | | Unknown. | ORGANISM U |
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| | | | KEYWORDS . |
| | | AR175898.1 GI:17917197 | VERSION A |
| | | AR175898 | ACCESSION A |
| | | Sequence 8 from patent US 63098/4. | DEFINITION S |
| F 21 F 7 5 5 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 7 6 | TTHEAT | AR175898 3636 DP UNA | LOCUS A: |
| DAT 17-DEC-2001 | 3.50 | | AR175898 |
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| SAAGAACTGCCTGGTGAAGAACCTG 1320 | 1 GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAA | 1261 | Db |
| | GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAAGGA | 1261 | γŞ |
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| 3GAAGGTTTGCTGGCCACCGTCACG 1260 | 1 ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGGA | 1201 | Q Q |
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| GCACGTGGCATCGTTGTGTACACT 1020 | ATTGCCTTCTTCTAACCAACTGTGTTGAAGGAACTGC | 961 | DB 4 |
| FGCACGTGGCATCGTTGTGTACACT 1020 | TELLO VATED LEGIZATO VA COLO MACCILLA LI | 961 | Ş |

| 3121 ACAGCTCTTGCTGCTGTGTCCTACTGCCCTGGGATGGGTGCAGCCCTTAGGATGTAT 3180 | 70 |
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| 061 AATTCTGTCTTCCAGCAGGGAATGAAGAACAAGATCTTAATATTTTGGCCTCTTTLGAAGAG | מת |
| 12 | δ. |
| .001 TTCTTTGTCAGTATCGTGGTAGTGCAGTGGGCTGACTTGGTCATCTGCAAGACCAGAAGG 306 | 40 |
| 001 TTCTTTGTCAGTATCGTGGTAGTGCAGTGGGCTGACTTGGTCAT | Q V |
| | Db 5 |
| 941 TACGGGCAGCAGTGGACCTACGAGCAGGGAAGATTGTGGAGTTCACCTGCCAC | S 5 |
| 94 | g 9 |
| ĊĊĊŢĠĠĠĠĠĠĠŢŦĊŦŦĊĀĊŦŦĀŦŦŦŦŦĠŦĠāĸŦſĠĠĠſĬĠĀĠĀĀĀĊĠĠĬĬĬĊĊĬĠĊſŎĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠ | Dβ |
| 2821 GCCTGGGAGGCTTCTTCACTTATTTTGTGATTCTGGCTGAGAACGGTTTCCTGCCCC111 2880 | \$ |
| 761 GACAAACTTGTGAACGAGCGTCTGATCAGCATGGCCTATGGACAGATCGGTATGATCCAG 282 | Db |
| ACAAACTTGTGAACGAGCGTCTGATCAGCATGGCCTATGGACAGATCGGTATGATCCAG 282 | 99 |
| 701 CTGGCCTATGAACAGGCTGAAAGTGACATCATGAAGAGGCAGCCCAGAAATCCCAAAACG 276 | DЬ |
| 701 CTGGCCTATGAACAGGCTGAAAGTGACATCATGAAGAGGCCAGCCA | Qy |
| 641 CTOSSCAPICSTSAPICATIONOTORATTGACTTGGGCACTGACATGGTTCCCGCCATCT | DЬ |
| 641 CTGGGCACCGTGACCATCCTCTGCATTGACTTGGGCACTGACATGGTTCCCGCCATCTCT 27 | ş |
| | , В |
| S81 AGTAACATTCCGGAAATCACCCCCTTCTTGATATTTATTF | Ş |
| | P |
| 521 GTAGAAGAAGGTCGTCTGATATTTGATAACTTGAAGAAATCCATTGCTTACACC | 2 ! |
| 61 1CC | B & |
| 461 TCCAAGCAAGCTGACATGATTCTTCTGGATGACAACTTTGCCTCCATCGTGACTGG | 5 5 |
| 46 | ? ? |
| 341 GIOGAGGETTETTGGCTCGGATGT | מע |
| 341 GTGGAGGGCTGCCAGCGGCAGGGTGCCATCGTGGCTGTCACAGGGGATGGTGTGCAATGAC 240 | y 9 |
| TGCGGTACCACACAGAATTGTCTTTGCTAGGACCTCTCCTCAACAGAAGCICAICAI | рь |
| 281 TTGCGGTACCACACGAGATTGTCTTTGCTAGGACCTCTCCTCAACAGAAGGTCATCATT | ş |
| 28 | B & |
| TOT CHETTARTACATGGCAGTGACTTGAAGGACATGACCTCTGAGGAGCTGGATGACA | ? 5 |
| 2161 GAAGACATTGCTGCCGCCTCAACATTCCAGTGAACCAGGTGAACCCCAGAGATGCCAGAGATCCAGTGAACCAGGTGAACCCCAGAGATGCCAAGATGCCAGTGAACCAGGTGAACCCAGAGATGCCAAGATGCCAAGATGCCAAGATGCCAAGATGCCAAGGTGAACCACGTGAACCCCAGAGAGATGCCAAG 2220 | \$ 5 |
| AAGGGGGTGGGCATTATCTCAGAAGGTAACGAGACCGTG 21 | |
| 101 ATCACAGCCAAAGCCATTGCTAAGGGGGTGGGCATTATCTCAGAAGGTAACGAGACCGTG 216 | VO 8 |
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Rat Na+,K+-ATPase alpha isoform catalytic subunit mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M14511
M14511.1 GI:203026
                                                                                                                                                                                                                                                                                                                                                                                Shull, G.E., Greeb, J. and Lingrel, J.B. Molecular cloning of three distinct forms alpha-subunit from rat brain Biochemistry 25 (25), 8125-8132 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATPase: integral membrane protein. Rat male brain (strain CD) cUNA to mRNA, clone B1-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                       Draft entry and computer-readable sequence of [1] kindly provided by G.E.Shull, 18-FEB-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus
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                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                       of the Na+, K+-ATPase
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Matches 3633; Conservative Query Match mat_peptide y Match 99.9%; Score 3631.2; Local Similarity 99.9%; Pred. No. 0; CCCCCTCCCACTACTCCCGAGT9995TCAAATTCTGTCG3CAGCTGTTCGGGTGGCTTCTCCC GGGAAGGGGTTTGGACGAGACAAGTATGAGCCCGCAGCTGTATCAGAACATGGGGACAAG 300 CASE CETAST TECONS CETTEN PART CONCORDED TO CART CT CON AGREE CONCORDED TO CONCORDE AAGAACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAGAAGATGAGCATCAAC ATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTACA 600 GACGACCATAAACTCAGCCTGGATGAACTCCATCGTAAATACGGAACAGATTTGAGCCGA 420 CAGCCTAGITICCCGCCTCTCGGCTCCCCCGGCTCCCACTCTCCCAGCCGGGAGCTGCTCT 180 GAAGAGGAACCACCAAATGATGATCTTTACCTCGGGGTCGTGCTGTCTGCTGTCGTCATC GGCCTAACACCCGCAAGGGCCGCTGAGATCCTGGCTCGGGATGGCCCCAACGCCCTCACG GGCCTAACACCCGCAAGGGCCGCTGAGATCCTGGCTCGGGATGGCCCCAACGCCCTCACG GACGACCATAAACTCAGCCTGGATGAACTCCATCGTAAATACGGAACAGATTTGAGCCGA 999AA99993TTGJACJAGACAASTATGASCCCGCAGCTGTATCAGAACATGGGGACAAG CTCCTCTTTCTAGTCTCCAGCCACAGGACCCGGCCGCGGGGGGCGCCACCATG GEAGCCTCGGCGEGAGGAGGCGGACACGTGGCAGCGGCGGCGGCAGCAGCAGCAGCG 60 ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAAAGCTCCAAGATCATGGAATCCTTC ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC GAAGAGGAACCACCAAATGATGATCTGTACCTCGGGGTCGTGCTGTCTGCTGTCGTCATC ATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTACA 89 bp upstream of NarI site 950 a /product="(Na+ and K+) ATPase, alpha catalytic subunit, mature peptide" a 958 c 995 g 823 t EGFQFDTDEWNFPUDNLCFVGLISMIDFPRAAVPDAVGKCRSAGIKVINVTGDHPITA
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GMGAALEMYPLKFTWMFCAFFYSLLIFVYDEVRKLIIRRRPGGWVEKETYY" GLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRMTVAHMW FDNQ;HEADTTENQSGYSFDKTSATWFALSRIAGELERAVRAGENLEILKRAVAGD ASESALLKCIEVCCGSWEMENKRYKTAVEIPRNSTUKYCLSTHKNPNASESKHLLVKGASPERILLKGLEVCGGSWEMENKENTKAVEIRAKTAVEIRAKTERAKTEKYEKGAPERILLKDEGFP 253. .3306 0; Mismatches E 566 DB 10; Length 3636; 3; Indels 0; Gaps 240 240 180 780 720 660 660 600 540 540 480 480 420 360 120 720 0

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| 1860 1860 | CTCCTCCACGGCAAGAGCAGCCCCTGGACGAAGAGACT | Db Qy |
|--------------|--|---------------|
| 1800 | AAGCACCTGCTAGTGATGAAGGGCGCCCAGAAAGGATCCTGGACCGAT | 95 95 |
| 1740 1740 | TTCAACTCCACCAACAAGTACCAGCTCTCCATTCA | Db 99 |
| σο σο | GTCTGCTGTGGCTCCGTGATGGAGATGAGGGAGAAGTACACCAAGATAGT | Oy Db |
| 1620 1620 | ATCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTG | Qy db |
| 1560 1560 | TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAA(| λδ 4 <u>α</u> |
| 1500 1500 | ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTT | P 64 |
| 1440 1440 | ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAJ | Db Oy |
| 1380 1380 | GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAAA | ОУ |
| 1320 1320 | GTATGICTGACGCTCACIGCCAAGCGCAIGGGGAGGAAGAACIGCCTGGIGAAGIIIIIIIIII | Db 2; |
| 1260 1260 | ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCG3AA35TTT19CTG3C0 | ДУ |
| 9 9 | CTGGGGGTGTCTTCTTCATTCTCTCTCTCATCCTTGAGTACACCTTGSCTCGAGGCTG | Оу |
| 1140 1140 | STGGCCGTGTTC | ОУ |
| 1080 1080 | GGGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCC | Db Qy |
| 1020 1020 | ATTGCCTTCTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACT | ₽ Q |
| 960 | TCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAAC | Db 97 |
| 900 | GATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTCA | Db Oy |
| 840 840 | GCAGAGGATGTCGTCGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCTGCT | dg VQ |

| 1 TACCGGCAGCAGTGGACCTACGAGCAGAGGAAGATTGTGGAGTTCACCT | ю ^U |
|---|----------------|
| 2881 CACCTGTTGGGG | 5 5 |
| 2821 GCCCTGGGAGGCTTCTTCACTTATTTTGTGATTCTGGCTGAGAACGGTT | д <u>0</u> |
| 2761 GACAAACTTGTGAACGAGCGTCTGATCAGCATGGCCTATGGACAGATCGGT | ā 8 |
| 2701 CTGGCCTATGAACAGGCTGAAAGTGACATCATGAAGAGGCAGCCCAGAAA | р 9 9 |
| 2641 CTGGGCACCGTGACCATCCTCTGCATTGACTTGGGCACTGACATGGTTCCCGG | g 9 |
| 2581 AGTAACATTCCGGAAATCACCCCCTTCTTGATATTATTATTATTGCAAACATTCC | 99 VQ |
| 2521 GTAGAAGAAGGTCGTCTGATATITGATAACTTGAAAGAAATCCATTGCTTACA | Db Oy |
| 2461 TCCAAGCAAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTCCATCGTC | DF 02 |
| 2401 TCTCCAGCTTTGAAAAAGGCAGATATTGGGGTTGCCATGGGGATTGTTGGCTCG | Db Qy |
| 2341 GTGGACGGCTGCCAGCGGCAGGGTGCCATCGTGGCTGTCACA(| 40 70 |
| 2281 TTGCGGTACCACACGGAGATTGTCTTTGCTAGGACCTCTCCTCAACAGAACGIIIIIIIIII | D OY |
| 2221 GCCTGTGTAGTACATGGCAGTGACTTGAAGGACATGACCTCTGAGGAGCTGGA | р У |
| GAAGACATTGCTGCCCGCCTCAACATTCCAGTGAACCAGGTGAACCCCGAGAGATG | 8 8 |
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| GCTGTGGGCAAATGCCGCAGCGCTGGGATTAAGGTCATCATGGTCACAGAGAGC | 90 |
| ACCICIGCITCGIGGGICTIAICICCAIGATIGACCCICCICGAGGIGCIGICC | 8 |
| ;acgaacagtttcccgaaggcttccagtttgacactgatgaagtcaatttcc | g & |
| ACCTAGAGCTGGGGGGCCTTGGAGAGCGTGTGCTAGGTTTCTGCCACCTCCTTC | Оу |
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                                                                                                                                                                                                           D10359 D00188
D10359.1 GI:220823
Na+, K+-ATPase alpha subunit precursor.
          Hara,Y. Nrayama,O., Kawakami,K., Nojima,H., Nagamune,H., Krojima,T., Ohta,T., Nagano,K. and Nakao,M.
Primary structures of two types of alpha-subunit of rat brain Na+,K+,-ATPase deduced from cDNA sequences
J. Ricchem. 102 (1), 43-58 (1987)
                                                                                                                                                                                                                                                                                 RATNKATP1 3407 bp Rattus norvegicus mRNA for Na+, P
                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                               Rattus norvegicus
                                                                                                                                                                                 clone.pRNKA11
                                                                                                                                                                                                                                                                  complete cds
88032933
                                                                                                               Rattus
                                                                                                                                               Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                               Rattus norvegicus (strain:Sprague-Dawley) brain cDNA to mRNA
                                                                                               (bases 1 to 3407)
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                                                                                                                               Rodentia; Sciurognathi; Muridae; Murinae;
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                              CCGAAGTGCTACAGAAGAGGAACCACCAAATGATGATGTACCTCGGGGTCGTGTGTC 647
                                                                                                                           CGGTGGCTTCTCCATGTTACTGTGGATTGGAAGCCATTCTTTGTTTCTTGGCTTATGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCGCCACCATGGGGAAGGGGGGTTGGACGAGAGAGAAGTATGAGCCCGGCAGCTGTATCAGA 64
CCGAAGTGCTACAGAAGAGGAACCACCAAATGATGTTGTACCTTGGGGGTTCGTGCTGTT
                                                                                                  CGGTGGCTTCTCCATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCAT
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                                                                                                                                                                                                                                                                                                                                                          AGATTTGAGCCGAGGCCTAACACCCGCAAGGGCCGCTGAGATCCTGGCTCGGGATGGCCC 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328
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IGMIQALGGFTYFVIJAENGFLPFHLLGIFFTMEDBWINDVEISYSGGMTYEGFKIV
EFTJETFAFWSIVVCGMEDLVICKTERNSVFGGMTSKILIFGLFEETALAAFLSYCG
GMGAALRMYPLKPTWWFCAFPYSLLIFVYDEVRKLIIFRFBGGWVEKETYY"
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RYHTEIVFARTSPOOKLIIVEGCOROGAIVAVTGDGVNDSPALKKADIGVAMGIVGSD
VSKOAADMILLDDNFASIVTGVEEGRLIFDNLKKSIAYTLTSNIPEITPFLIFIIANI
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ASESALLKCIEVCGSVMEMERYTK.VEIPRISTRYKYQLSIHZIPNASEDHHLVMK
GAPBRILDRGSSILHGKEQPLDEELKDAFQNAVLELGGERVLGFCHLLLDPBGFP
EGFQFPTDEVNFPVDNLCFVGLISMIDPPPAAVPDAVGKCRSAGIKVIMVTGDHPITA
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LEGGQTPIAEEIEHFIHLITGVAVFLGVSFFILSLILEYTWLEAVIFLIGIIVANVPE
GLLATVTVCLTLTAKRMARKNCLVKNLEAVETUGSTSTICSDKTGTLTQNRMTVAHMW
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KLSLDELHRKYGTDLSRGLTPARAAELLARDGRALTPPTTDEWVKFCRQLFGGFSK
KLSLDELHRKYGTDLSRGLTPARAAELLARDGRALTPTTGCFSYYQEAKSSKIKES
LLWIGAILCFLAYGIRSATEEEPFIDDLYLGVVLSAVVIITGCFSYYCEAKSSKIKES
FXDMVPQQALVIRNGEKMSINAEDVVVGDLVEVKGGDRIPADLRIISANGCKVDNSSL
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881 c 913 g 791 t
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/protein_id="BAA01189.1"
/db_xref="GI:220824"
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/db_xref="taxon:10116"
/clone="pRNKA11"
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| AAAGTGCATCGAGGTCTGCTGTGGCTGCGTGGCTGATJAGAGTAGAGJAGAAGTACACCAAGAT I | п п |
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| CTGGTTCG-T-T-T-CAGAATTGCTG-STCTCTGTAACAGGGAAGTGTTTCAGGCTAACCA 1 | p 14 |
| CCATGAAGTTGATATTACAGAGAGAAGTGAGAGTGAGGTCTCCTTTGACAAGACGTCAGCCAC 1 | F-4 F-4 |
| GACTGGAACTCTGACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAAT 1 | p-4 p-4 |
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| 066 GRAGRAMARAMENA MANAMENTANTAN BARBARAN BARBARAN BERTARAK BARBARAN BARBAR | ٠ |
| 0)6 GGTTGTGTACACTGGGGATGGCACGTGATGGGCACCCTTGGCACCCTTGCTTCTGGGCT 1067 | F- |
| 948 93A3ACAA93AACAFTSOCTTOTTOTOAACCAACTGTSTTGAA93AACTGCACGTGGCAT 1007 | |
| 88% ACTOACTSSTSAAIOASAAOOOGASACTOSSTCOCOSSATTTOACAAAOGAGAACCCCTT 947 | |
| ### ODJAATOOJTSCTGATOTOAJAATGATATOTSGAAATSSCTGCAAGGTGGATAACTCCTC 887 | |
| 7%8 GATGAGCATCAACGCAGAGGATGTCGTCGTTGGTGGTGGTGGAGGTGAAGGGCGAAGA 827 | |
| 708 CATGEAATECTTCAAGAACATGETCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAGAA 767 | |
| 648 TGCTGTCGTCATCATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGAT 707 | |

| , | Db 2 | - ' | Db 2 | | | | - | | Qy 2 Db 2 | | | | Оу 2 Db 1 | | Qy 1 Db 1 | Qy 1 Db 1 | , , | Db 1 |
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| 2808 CGGTATGATCCAGGCCCTGGGAGGCTTCTTCACTTATTTTTTGAT | 2748 AAATCCCAAAACGGACAAACTTGTGAACGAGCGTCTGATCAGCATG | 2688 TOCOGOATCTCTCTGGCCTATGAAAGGCTGAAAGTGACATG | 2628 CATTCCACTSCCCCTGGCCACCSTGACCATCCTCTGCATTGACT | 2568 TTACACCCTAACAAGTAACATTCCGGAA | 2508 CATCUTSACTSSASTASAAGAASSTCSTCTGATATTTSATAACT | 2448 TGGTTCGGATGTSTCCAAGCAAGCTGCHGACATGATTCTTC1934 | 2388 TƏSTÜTCAATGACTCTCCASCTTTGAAAAASSCASATATTO | 2328 GAAGCTCATCATTGTGGAG3GCTGCCAGCGGCAGCGGCAGCGGCAGCGGCAGCGGCAGCGGCAGCGGCAGCGGCAGCGGCAGCGGCAGCGGCAGCGAGCGGCCAGCGAGCGGCCAGCGAGCAGC | 2268 GCTGGATGACATTTTGCGGTACCACACGGAGATTGTCTTTGCTA | 2208 CAGAGATSCCAAGGCCTGTSTAGTACATSSCASTSACTTSAAGGAC | 2148 TAACGAGACCGTGGAAGACATTGCTGCCGGCCTGAACATTGCAGTG | 2088 AGENGACCATCCAATCACAGCCAAAGCCATTGCTAAGGGGGTGGGG | 2028 TGCTGTCCCCGATGCTGTGGGCAAATGCCGCAGCGCTGGGATTAAG | 1968 TYTCCCCGTGGATAACCTCTGCTTOGTGGGTCTTATCTCCATGATT | 1908 COTOCITOTGCCTGACGACAGITTCCCGAAGGCTTCCAGITTGAC | 1848 CTTTCAGAATGCCTACCTAGACCTGGGGGGGGGGCTTGGAGAGCGTG | 1788 ATGCAGTTCTATCCTCCTCCAC23CAA33A3CA3CCCTT93A | 1505 CHILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII |
| TCTGGCTGAGAACGG 2867 | 9900TATGGACAGAT 2807 9900TATGGACAGAT 2584 | ATGAAGAGGCAGCCCAG 2747 | TOGGCACTGACATGGT 2687 TGGGCACTGACATGGT 2464 | ATTTATTATTGCAAA 2627 ATTTATTATTGCAAA 2404 | | NIGAPAACTITGOCTO 2507 NTONCARCITITGOCTO 2284 | CATGGGGATTGT 2 'A1GGGGATTGT 2 | | COTOTOGTOAACA 23 | CATGACCICIGAGGA 2267 | 3AACCAGGTGAACCC 2207 3AACCAGGTGAAAACC 1984 | CATTATCTCAGAAGG 2147 ATTATCTCAGAAGG 1924 | STCATCATGGTCAC 20 STCATCATGGTCAC 18 | TGACTCTCCAGC 2027 | ACTGATGAAGTO ACTGATGAAGTO | 3CTAGGTTTCTGCCA 1907 | AGAGCTGAAGGACGC 1847 AGAGCTGAAGGACGC 1624 | |

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                                                                                                                                                                                                                                                                                         RNATPAR RATE Alpha subunit kidney-type Na+,K+-ATPase.
                                                                                                                                                 Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                 X05882 D00188
X05882.1 GI:55771
              Hara,Y., Urayama,O., Kawakami,K., Nojima,H., Nagamune,H., Kojima,T., Ohta,T., Nagano,K. and Nakao,M. Primary structures of two types of alpha-subunit of rat brain Na+,K+,-ATPase deduced from CDNA sequences
                                                                                                                                                                                                                      Rattus norvegicus.
J. Biochem. 102 (1), 43-58 (1987)
                                                                                                           (bases 1 to 3407)
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                                                                                                                      | CCGAAGTGCTACAGAAGAGGAACCACCAAATGATGATGATCTGTACCTCGGGGTCGTGCTGTC
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                                         TGCTGTCGTCATCATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGAT
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FKNMYPQQALVIRNGEKMSINAEDVVVGDLVEVKGGDR IPADLRI ISANGCKVDNSSI
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GLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNEMTVAHMM
PDNQIHBADTTENQSGVSFDKTSATWFALSRIAGLCHRAVFQANQENLPILKRAVAGD
ASESALLKCIEVCGSVMEMFEKYTKIVEI FENSTNKYQLSIHKNPNASEPKHLVMK
GAPERILDRCSSILLHGKKEQFDLDEELKDAFQNAYLELGGLGERVLGFCHLLLPDEQFF
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RYHTEIVFARTSPQQKLI IVEGCQRQGAI VANTGDGVNDSPALKKADI GVAMGI VGSD
VSKQAADMI LLDDNFASI VTGVEEGRLI FDNLKKADI GVINI PEI TPFLI FIL
PLPLGTVTI LCIDLGTDMVPAI SLAVEQAESDIMKYPQPRNPYTDKLVNEPLI SNAYGQ
IGMIQALGGFFTYFV LLAENGFLPFHLLGI RETWDDRWINDVEDSYGQQMTYEQRKI V
EFTCHTAFFVSI VVVQWADLVI CKTRRNS VFQQGMXKKI LI FELFETALAAFI.SYCP
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881 c 913 g 791 t
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99.3%; Pred. No. 0;
vative 0; Mismatches
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| 1787 1564 | CSCATCSSAGOTTAASCAOTISCTAGTSATSAAGGGGGGCCCAGAAAAGGATCCTGGACO | 유 동 |
| 1727 1594 | ASTSSASAITOOOTITSAACIYOOACAACAASTACCASCITCTCCATTCACAAGAACCCAA | 8 |
| 1667 1444 | ARAGIGEATOSAGGICTSCTSTSGCTCOSTGATGSAGAGSAGGSAGGAAGIACACCAAGA | 용 상 |
| 1607 1384 | ASAAAACCTGCCTATCCTTAAGCGTGCAGIAGCGGGAGATGCTTCCGAGICGGCGCTCTC | 용성 |
| 1547 1324 | CISSITOSCE TOTOCASAAITSCESSICICTSIAACASSSCASTGIITCASSCIAACCI | 음 성 |
| 1487 1264 | CCATGAAGCTGACACCACAGAGAAICAGAGIGGGGGGGGGTCAGCCAC | Ûγ |
| [1427 1204 | 1368 FANTGRAANTETSACTEASAACESSANGACASTGGCTCACATGTGGTTTGACAATCAAAT | g, Q |
| 1367 1144 | GRTSAAGAAGGTGAAAGGTGBGAGAAGGTTGBGGGGCACATCCACCATCTGCTCCGACAL | 유 성 |
| 1307 1084 | GSCYACYSTYACGSTATGTCTGACGCTCACTGCCAAGGGCATGSCGAGGGAAGGAAGAACTGCCT | β ξ |
| 1247 1024 | GERGAGGERGICATOITOITOATEGGTATVATOGTAGCCACGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | 유 상 |
| 1187 964 | | 5 5 |
| 1127 904 | ggaaggogscetgacooccattgetgaagaaatogagcacttcatccacctcatcaogg | 9 5 |
| 1067 | CSTTGTGTACACTGGGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCT | λς Ας |
| 1007 | GSAGACAAGGAACATTGCCTTCTCTCTAACCAACTGTGTTGAAGGAACTGCACGTGGCAT | å Ö |
| 947 724 | actoactostsaatcasaacoccasactosstoccossattecacaaacsasaacoccti | λ. δ |
| 887 | COSAATOOTIGOTIGATOTICASAATICATATOTISCAAATISSCTIGGAAGSTISSATAAGTOCTIGOTIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 95 |
| 827 604 | GATGAGCATCAACSCAGASSATSTAGTCGTTGGTGGTGATCTGGTSSAGGTSAAGGGTGAAGGGTGAAG | 8 8 |
| 767 544 | OATOGAA (OCTITAAO)AATATOTETOTECANTAGOTETCGESATECGAAAEGSAGAAA | P 5 |

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Mus musculus, clone MGC:37763 IMAGE:5096872, mRNA, complete
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                                                                                                    Submitted (11-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892·2590,
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Contact: MGC help desk
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  Tissue Procurement: Jeffrey E.
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                      cgapbs-r@mail.nih.gov
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Series: IRAK Plate: 57 Row: b Column: 4.
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LEGGQTPI ABEI EHFIHLI TGVAVFLGVSFFI LSI I LEYTWLEAV I FLI GIVANVPE
ELLATVUCLTLYAKRMARKKCLVKHLEAV HETIGSTESTI CSSKTGTLTQNRMTVAHMW
FDNQI HEADTTENQSGVSFDKTSATWFALSR I AGLCNRAVFQANQENLP I LKRAVAGD
ASESALLKCLEVCCGSVMENREKYSKI VEI PENSTNKYQLSI HKYNDNASEPKHLLVMK
GAPERI LDRCSS I LLHGKEOP LDEELKDAFQNAYLELGGLEBRVLGFGHLLLPDEOFP
EGFQPDTDDVNFPVNICFVGLI SMI DPPRAAVPDAVCKCRSAGI KVI MVTGDHPI TA
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IGMI QALGGFFTYFVI LAENGFLPFHLLGI REFMDDRWVDI T ERI FEFTAN A NET GVCD
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GMGAALRMYPLKPTWWFCAFPYSLLIFVYDEVRKLIIRRPGGWVEKETYY"
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KLSLDELHRKYGTDLSRGLTPARAAEILARDGPNALTPPPTTPEWVKFCRQLFGGFSM
LLWIGAILCFLAYGIRSATEEEPPNDDLYLGVVLSAVVIITGCFSYYOEAKSSKIMES
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/protein_id="AAH25811.1"
/db_xref="GI:19387931"
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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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| #POTTOCTCATT03TATCATC3TA3CCAACSTC0C93AAS3TTT95TG8CCACGTCACG | 1201 A 1194 A | , B 5 |
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| ACCONTATTSTTSAASAAATOGASJACTTCATCCACCTCATCACGSGTGTGGCCGTGTTC | 1081 A 1074 A | φq |
| -999ATP99CACPSTGAT9999CAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCCTG | 1021 6 | da da |
| ATTGCCTTCTTCAACCAACTGTGTGTGAAGGAAACGGACAGGGCATCGTTGTGTACACCT | 45 4 A | 5 S |
| 901 TUAGAACUUCAJACTOGSTOOCOGSATTTCACAAACSAGAACOCCTTGGAGACAACAASGAAC 960 | 901 T 894 T | g V |
| 841 GATCTCK-JAATCATATCT-CCAAATSSCTGCAAGSTSSATAACTCCTCACTCACTGSTGAA 900 | 834 G | Db dq |
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| 721 AMBANCATPSTECKTTCASKAASKNOTCHTSATTCSAAATHYAMANAAGATYAMSCATCAAC 780 | 721 A 714 A | qa Að |
| 561 ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC 720 | 554 A | qq |
| 501 GAMGARGAACCACCAAATGATGATGTSTACCICGGGGTGTGTGTGTGTGTGTGTCATC 660 | 5 6 6 1 4 1 3 - 0 | d Ç X |
| 541 ATGITACTGT93ATTG3A3CCATTCTTTGTTTGTT3GCTTATGGCATCCGAAGTGCTACA 600 | 541 A 534 A | qq VQ |
| 481 CCCCCCCCCCACTACTCCCGAATGGGTCAAATTCTGTCGGCAAGCTGTTCGGTGGCTTCTCC 540 | 481 C 474 C | pb Qy |
| 421 GGCTTAACACCCGCAAGARCGCTDAAGATCTTRACTTGAGATGGCCCCAACGCCCTCACG 480 | 421 G | д Су |
| 361 GACGACCATAAACTCAGCCTGGAIGAACTCCATGGTAAATAGGGAACAGATTTGAGCCGA 420 | 361 G | 40 |
| 301 AARAGCAASAAGGCSAAGAAGGAAAGGSACATGGACGAACTCAAGAAGGAAGTGTCTATG 360 | 301 A 294 A | B 5 |
| GOGANGTOGGTTGGACGAGACAAGTATGAGCCCGCAGCTGTATCAGAACATGGGGACAAG | 241 G 234 G | 문 왕 |

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3474 GUCGGGGGAAGGGTTGACTGAGAAACACCGTGTACGGGGACGACAGCGGGCAAGGTTTA 3533
                                          3479 ----- GOGGGGAGGGCTGCCGGAAAAACACCGTGGACGGGGACGACAGCGGGGAAGGTTTA 3534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J. C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touthman, J.F., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, M2 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gc
Series: IRAK Plate: 55 Row: 9 Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamor frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaithersburg, Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nouse mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        web site: http://www.nisc.nih.gov/
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                                                                                                                                                                                                                                                                 /tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                           /product="ATPase, Na+K+ transporting, alpha 1 polypeptide"
/protein_id="AAH21496.1"
/db_xref="GI:18204493"
/db_xref="GI:18204493"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                     /clone="MGC:38419 IMAGE:5346159"
                                                                                                                                                                                                                                                                                                                                                                                                /map="FVB/N"
translation="MGKGVGRDKYEPAAVSEHGDKKGKKAKKEPDMDELKKEVSMDDH/
                          /db_xref="LocusID:24211"
                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                             ATAACTFGCTSTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC
                                                                                                                                                                                                                                                          GGATTAACACTTGCAAGGGCCGCTGAGATCCTGGCCCGGGGATGGCCCCAACGCCCTCACA
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EGFYFDITCVNEPVONLCFVGLISMIDFPRAAVPDAVGKCESAGIKVIMVTGDHPITA
KAIAKGVGIISEONETVEDIAARLIN PNQVNEPDAKKOVHGSDLKOMTSEELDDIL
PYHTSIVFARTSVGYGLIIVEGGGFYGAILOFNTGGGWNESFALKKAIKKACHGAWGIVGSI
VSQAADMILLDDNFASI VTGVEGGRLIFDNLKKSIAYTLTSNIPEITPFLIFIIANI
FLEGITTILITGTTMVPAISLAVECAESDIMKFGPRWNDVBSSYGQQWTYQOKIIV
COMIQALGGFFTYFVILAENGFLPFHLIGIRETWDDRWNDVBSYGQQWTYQOKICMIQALGGFTTYVILAENGFLPHLIGIRETWDRWNDVBSYGGQWTYQOKICMIQALGGFTTYVILAENGFLPHLIGIRETWDRWNDVBSYGGQWTXQOKICMICHTHANAFISYGP
GMGAAIRWYPLKTTWWFGAFPYSLLIFYDDEVFKLIIFRRPGGWVEKETYY"

GMGAAIRWYPLKTTWWFGAFPYSLLIFYDDEVFKLIIFRRPGGWVEKETYY"

GMGAAIRWYPLKTTWWFGAFPYSLLIFYDDEVFKLIIFRRPGGWVEKETYY"

GMGAAIRWYPLKTTWWFGAFPYSLLIFYDDEVFKLIIFRRPGGWVEKETYY"
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LLWIGAILCELAYGIRSATEEEPPNDDLYLGVVLSAVVIITGCFSYYQEAKSSKIMES
FKMWPQQAIVIPNGEKMSINAEDVVVVGDLVEVKGGDRIPALRIISANGCKVDNSSL
TGESEPQTRS PPFTNENPLETPNIA FFSTNCVEGTAPGIVVYTGDPTVNSPIATLASG
LEGGQTDIAEE EHFIHLITGVAVFLGVSFFILSLILBYTWLEAVIFLIGIIVANVPE
GLLATVTVCLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRMTVAHMM
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ASESALLKCIEVCCGSVMEMREKYSKIVEIPFNSTNKYQLSIHKNFNASEPKHLLVMK
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| 1741 ANGENEETGETAGTGAAGGGGEGCECAGAAAGGATECTGGAACGGATGCAGTTETATE 1800 | Qy Db |
| 1687 TECANCTOCACCAACAAGTACCAGETCTCCATTCACAAGAACCCAAACGCATTCGGAGCCT 1740 | Db Cy |
| 1621 GTCTGCTGTGGCTCCGTGAT9JAGATJAG9GAGAAGTACACCAAGATACTGTGAGATTCCC 1680 | og og |
| 1561 ATCCTTAAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAG 1620 | ДУ |
| 1501 TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTTAACCAGAAAACCTGCCT 1560 | Qy db |
| 1441 ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGGCAGG | DB 53. |
| 1381 ACTCAGAACCGGATSACAGTGGCTCACATGTGTTTTGACAATCAAATCCATGAAGCTGACTGA | Db Cy |
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| 967 ATTSCCTTCTCCAACCAACTGTGTGGAAGGAACTGGAAGTGGAGATGGTGGTGGTACACT 1020 | Ep Gy |
| 901 FOAGAACCCCAAACTCGGTCCCAGGATTTCACAAACGAGAAAACCCCTTGGAGACAAGGAAA 960 | Å å |
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                     ATATCTGGATTTTTACAAATAAAGATGGCTATTATAACGGAA 3636
                                                                                                                                                                                                        CCAAAGCATGTGGGGATCCAGACGTCCTG5AATGAAGCATGTAGCTGTAATGGSGGGC-- 3478
                                                                                                                                                                                                                                                                      TACCCCCCTTTGTGTACTTCAAGTCTTGGAGCTCGGAACTCTACCCTGGTAGGAAAGCA 3420
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ATATCTGGATTTTTACAAATAAAGATGGCTATTATAACGGAA 3648
                                                                             TATGTGCCTTTTTGTTTTTGTAAAAAAGGAAAACCTGGAAAGACTGAAAGATTACGTTTT
                                                                                                                         GGCGGGGGGAGGGCTGCCTGAGÀAACACCGTGTACGGGGACGACAGCGGGCAAGGTTTA
                                                                                                                                           ----GGGGGGAGGGCTGCCCGAAAAACACCGTGGACGGGGACGACAGCGGGGAAGGTTTA 3534
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SOURCE
ORGANISM
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                                                                                                KEYWORDS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                  Mus musculus
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house mouse

RESULT 10 BC025618 LOCUS DEFINITION ACCESSION Mus musculus, clone MGC:38134 IMAGE:5320976, mRNA, BC025618 BC025618 GI:19343735 MGC complete cds. POD 07-AIIG-2002

REFERENCE AUTHORS TITLE JOURNAL Strausberg, R.

(bases 1 to 3686)

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2887 CACCTGTTGGGCATCCGAGAGACCTGGGATGACCGCTGGGTCAACGATGTGGAGGACAGC

2946

COMMENT PEMAPK Direct Submission
Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, COLLEGE: Email: cjapbs rëmail.nih gov Tissue Procurement: Jeffrey Green M.D. Tissue Procurement: Life Technologies, NIH-MGC Project URL: ht Contact: MGC help desk http://mgc.nci nih.gov Inc.

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BASE COUNT
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Series: IPAK Flate: "6 Pow: f Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency OFF
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Contact: nisc_mgdshBgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Allakesley,R.W., Bruffard,G.G., Breen,K., Brinkley,C., Brocks,S.,
Blakesley,R.W., Bruffard,G.G., Breen,K., Brinkley,C., Brocks,S.,
Blakesley,R.W., Bruffard,G.G., Breen,K., Brinkley,C., Brocks,S.,
Hansen,N., Ho.S.-L., Karlins,B., Kwong,P., Laric,P. Legaspi,R.,
Maduro,Q.I., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.T., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Charg,L.. H. and Green,E.S.
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T3ESEP-JESELGHTHENELIRNIAFF SINCVETTAGIA VVTT-JDRTWASELATLAS-G
LEGGGTFIAESELEHTHELITGVAVELGVEFTELSLIERTWERAVIFLIGIIVANVBE
GLLATVTVCLTLTAKPMARKNCLVKNLEAVETLJSTSTICSDKTOTLT-JNEMTVAHMM
FDNOHEADTTENOSGVSFDKTSATWRALSRIAGLCNRAVGANGENLFIKRAVAGD
ASESALLKCIEVCOJS VMEMBEKYSKIVELPENSTNKYGLSIHKNENASEVHLLVMK
GAPERILDROSSILLHGKEOPLDEELKOAF GNAYLELGGLGERVUGFCGLLLDDEOGF
BGFOFTTDDVKPPVDNLCFVGLISMIDPPRAAVPDAVGKCRSAGIKVLMVTGHHFITA
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EFTCHTAFFVSIVVVQWADLVICKTPPNSVFQQЭMKNKILIFSLFEETALAAFLSYCF
GMGAALRMYPLKPTWWFCAFPYSLLIFVYDEVRKLIIPRRPGGWVEKETYY"
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/protein_id="AAH25618".1"
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PYHTEIVFAPTEPQKLIIVEGGGPGGAIVAVTGGSVMDSPALKKADIGVAMGIVGSD
VSKQAADMILLDDNFASIVTOVEGERLIFUNKKSIAYTLTSNIPEITPEIFIIAU
PLPLGTVTILCIDLGIDMVPAISLAYEGAESDIMKRGPPNFYTDYLVNEPLISMAYGG
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ductal carchoma. 5 month old virgin mouse."
/cione_lib="NC1_CAP_Mam6"
/lab_host="DH10B"
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| GATGTCAATTTCCCCGTGGATAACCTCTGCTTCGTGGGTCTTATCTCCATGATTGACCCT 203 | Db |
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| AACCCAAACGCATCGGAGCCTAAGCACCTGCTAGTGATGAAGGGCGCCCCAGAAAGGATC | ογ |
| AGCAAGATAGTGGAGATTCCCTTCAACTCCACCAACAAGTACCAGTTGTCCATTCACAAG 1 | Db |
| ACCAAGATAGTGGAGATTCCCTTCAACTCCACCAACAAGTACCAGCTCTCCATTCA | ογ |
| GCGCTCTTAAAGTGCATTGAAGTCTGCTGCGGCTCCGTGATGGAGGTGAGGGAGAAATAC 167 | Db 4 |
| ология в метериория в пред пред пред пред пред пред пред пред | 2 |
| 1540 GCTAACCAAGAAAACCTGCCTATCCTTAAGCGTGCAGTAGCGGGGAGATGCTTCCGAGTCG 1599 | dd VQ |
| TCAGCCACCTGGTTCGCTCTGTCCAGAATTGCTGGTCTCTGTAACAGGCAGTGTTTCAG 1 | Db |
| TCAGCCACCTGGTTCGCTCTGTCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAG 15 | 9 |
| AATCAGATCCATGAAGCTGACACCACGGAGAATCAGAGTGGTGTCTCCTTTGACAAGACG 149 | Db C |
| ANTOAAATOOATGAAGOTGACAGAGAGAATGAGAGTGGGGTCTCCTTTGACAAGAGG 147 | |
| TCAGACAAGACTGGAACTCTGAC | γ γ |
| ACTGCCTGGTGAAGACTTGGAAGCTGTGGAGACCTTGGGGTCCACATCTACCATCTGC 13 | ф |
| ACTGCCTGGTGAAGAACCTGGAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTG | Qy |

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                                                                                                                                                                                                                                                                                                             through the I.M.A.G F. Consortium/LLNL at http://image.llnl.
Series: IPAK Plate: 56 Pow: g Column: 14
This clone was selected for full length sequencing because it
                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisC mgc3nhgri.nih.gov/
Akhter, N. Ayele, K. Percetrom-Sternberg, S. M. Banjamin, B.
Akhter, N. Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P. Legaspi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P. Legaspi, P.,
Maduro, M., Masiello, C., Maskeri, B., Maertian, S. L., McCloskey, J. C.,
McDowell, J., Pearson, B., Stantipop, S., Thomas, P. J., Touchman, J. W.,
Tsurgeon, T., Voy, J. L., Walker, M. A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-ramail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by The T.M.A.G.E. Conserva-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project UPL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (of JTN 2002) Mational Institutes of Health, Mammalian Gene Collection (MBC), Cancer Genemics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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MAGS musculus, hypothetical protein MGC28413,
MAGE:5321268, mRMA, complete cds.
                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G E. Consortium/LLNL at http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by. Mational Institutes of Health Intramural Sequencing Center (NISC),
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                              passed the following selection criteria: Hexamer frequency ORF
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                                                    /Cloue="MGT vw14E IMAGE.5211268"
/tissue_type="Mammary tumor. C3(1)-Tag model. Infiltrating ductal darchroma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/tab_lib="CHIPE"
                        /nore="Vector: pCMV-SPORT6"
                                                                                                                                                                     /map="FVB/N"
                                                                                                                                                                                                            /organism="Mus musculus"
/codon_start=1
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301 AASAGCAAGAAGAAGSAAGSAAAGSGACATGGACSAAGTCAAGAAGSAAGTGTCTATG
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FDNQHEADTTENQSGVSFEKTSAMWEALSELASTSTICSDKTSTITQNBMIVAHMM
FDNQHEADTTENQSGVSFEKTSAMWEALSELASTCHQANQENLEFILKAVAGD
ASESALLKCIEVCGGSVMEMREKYSKIVELIFNSTMYVQLGIHENDAGEFHHLLVK
GAPERILDRCSSILLHGKEQPLDEELKDAFQNAXLELGGIGERVLGFCHLLLPDEOFP
EGEFOFDDUNFPUNNLCFVGLISMIDPRAAVPDAVGKCRSAGIKVIMTTGDHPITA
KAIAKVGGISEGNETVEDIAARLNIFVNQVNPRBAKACVVHGSDLKDMTSEELDDIL
PXHTELVHARPSFCMELIIVESCQRGANIVAVTGDGVNDSPALKADIGVAMGIVGSD
VSFQAADMILLTCHDNFASIVTGVEEFFLIFDNLKESIAYTLTSNIFEIIFFLIFIIANI
PLFLGTVTILCIDLGTDMVFAISTAVEDAEGNIKMFTGTENDEVISMAVGQ
IGMIGALGGFFTYFVILAENGFLPFHIGTFETGTETDAWNTLLIFGLFEETALAAFLSYCP
SMGAALFMYPLFTMRFTAFFYSLIFUNGFGFMYNKLIFGLFEETALAAFLSYCP
GMGAALFMYPLFTMRFTAFFYSLIFUNGFGFFFFIIFFPPGGMVEKETXY"
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TGESEFGTF&FDFINEMFLETEMIAFFSTHCVEGTAPGIVVYTGDPTVMGPIATLASG
LBGGQTPIAEEIEHFIHLITGVAVFLGVSFFILSLILEYTWLEAVIFLIGIIVANVPE
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| KLSLDELHRKYGTDLSRGLTPARAAEILARDGPNALTPPPTTPEWVFFCPQLFGGFSM
| LLWIGAILGFLAYGIPSATEEEPPNDDLYLGVVSAVVIITGCFSVYQEAKSSKIMES
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/protein_id="AAH32187.1"
/db_xref="d1:21595127"
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| COLUMN CONTRA LA COLUMNA DE LA COLUMNA | ? |
| 521 GTCTGCTGCGGCTGATGAGAACAGGGAGAAAATACAGCAAGATAGTGGAGATTGCC 173 | 5 S |
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| 557 TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTGCC1 101 | DЬ |
| 01 TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTGCCT 15 | γQ |
| 97 ACCACGAGAATCAGAGTGGTGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTG 155 | ДĎ |
| 41 ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTG 15 | 9 |
| 37 ACTCAGAACCGGATGACAGTGGCCCACATGTGGTTTGACAATCAGATCCATGAAGCTGAC 149 | DЬ |
| 81 ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTTGACAATCCATGAAGTCGAC 14 | Qy |
| 77 GAAGCTGTGGAGACCTTGGGGTCCACATCTACCATCTGCTCAGACAAGACGGGAACTCTG 143 | dd |
| 21 GAAGCTSTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG 138 | γÇ |
| 17 GTCTGTCTGACACTCACTGCCAAGCGCATGGCGAGGAAGAACTGCTGGTGAAGAACTTG 1 | qa |
| 61 GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCTG 132 | Qy |
| 57 ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCAGAAGGTCTGCTGGCCACTGTCACG 1 | DЪ |
| 01 ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCACG 126 | γQ |
| 97 CTGGGGGTGTCTTCTTCATCCTTTCTCTGATCCTTGAGTACACCTGGCTCGAGGCTGTC 12 | Db |
| 41 CTGGGGGTGTCTTTCTTCATTCTCTCTCTGATCCTTGAGTACACCTGGCTCGAGGCTGTC 120 | , 9 |
| 37 ACCCCCATTGCTGAAGAGATTGAGCATTTCATCCACCTCATCACCGGGGTGGCCGTGTTTC | dd |
| B1 ACCCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTTC 114 | γQ |
| 77 GGGACCGCACCGTGATGGGCAGGATTGCCACGCTTGCCTCTGGGCTAGAAGGTGGC | рь |
| 21 GGGGATGGGAACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCCTG 10 | γΩ |
| 17 ATTGCCTTCTTCTAACCAACTGTGTGGAAGGAACCGCACGTGGCATCGTCGTGTACACT | дb |
| 11 | γQ |
| ACCCCTTGGAGACAAGGAAC 10 | g 99 |
| ;ATCTTAGAATCATATCTGCAAACGGCTGCAAGGTGGATAACTCCTCACTCA | DЬ |
| ATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTCA | γQ |
| ;cggaggargrcgrcgrcgaggarcregrggaggrgaaaggggagaccggarcccrecr | Db |
| -ÿ | γQ |
| AGAACATGGTCCCTCAGCAAGCCCTTGTGATTCGAAATGGAGAGAAAATGAGCATCAAT 8 | Db |
| AGAACATGGTCCCTCAGCAAGCCCTTCGTGATTCGAAATGGAGAGAAGATGAGCATC | 0. |
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                   Submitted (UE:MAN 2002) Matternal Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Poom 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                           Mus musculus
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Clone distribution: MSC clone distribution information can be found through the I M A G E. Consortium/IIML at http://leage.llnl gov Series: IRAF Plate: 56 Pow: f Column. 24
This clone was selected for full length sequencing because it passed the following selection criteria. Hexamer frequency ORF
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Contact: MGC help desk
Email _ cgapks-r@mail.nih_gov
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Contact: nisc_mgc@nhgri nih.gov
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Tissue Procurement: Jeffrey Green M.D.
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/tissue_type="Manmary timor C3(1)-Tag model.
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| CACTCACTGGTGAA 90 CACTCACTGGTGAA 90 | GATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGG | ОУ |
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| AGATGAGCATCAAC 78 | AAGAACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAJ | Oy Db |
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| TGCTGTCGTCATC 66 | GAAGAGGAACCACCAAATGATGATGTGTACCTCGGGGTCGTG | dg VQ |
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| сстстттестессвевы 12 | ;caacAacAacaaccaaccrcaarccaaaacacccaaccsrccrc | Db |

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| 63 63 | GAAGACATTGCTGCCCGCCTCAACATTCCAGTGAACCAGGTGAACCCCA | | |
| 216 216 | CAAAGCCATTGCTAAGGGGGTGGGCATTATCTCAGAAGGTA gaaagcCattgcCaaggggTaggCattatCtCAgaaggCa | | |
| 210 | GCTGTGGGCAAATGCCGCAGCGCTGGGATTAAGGTCATGATGGTCACAG | | |
| 2046 | AACCTCTGCTTCGTGGGTCTTATCTCCATGATTGACCCTCCTCCAGCTGC | | |
| 1980 1986 | GACGACAGTTTCCCGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTT | | |
| 1926 | TACCTAGAGCTGGGGGGCCTTGGAGAGCGTGTGCTAGGTTTCTGCCACCT | | |
| 1866 | CTCCTCCACGGCAAGGAGCAGCCCCTGGACGAAGAGCTC | | |
| 1800 | AAGCACCTGCTAGTGATGAAGGGCGCCCAGAAAGGATCCTGGACCGATG | | |
| 1740 | TTCAACTCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCTIIIIIIIIII | | |
| 1680 1686 | GTCTGCTGTGGCTCCGTGATGGAGATGAGGAGAAGTACACCAAGATAGT | | |
| 1626 | ATCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAGTCTTAAAGTGCATCGAGTCGGCGCTCTTAAAGTGCATTGAAAGTGCATTGAAAGTGCATTGAAAGTGCATTGAAAGTGCATTGAAAAAGTGCATTGAAAAAAAA | | |
| 1566 | TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAGAAAACCTGCCT | | |
| 1500 | ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTG | | |
| 1446 | actcagaaccggatgacagtggctcacatgtggtttgacaatcaaatcacatgaagctgac | | |
| ساسا | GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCT | | |
| 2 2 2 | TCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACC | Qy 126 Db 126 | |
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Rattus norvegicus brain and liver, cDNA to
Rattus norvegicus
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Rattus morvegicus Na,K-ATFase alpha 1 subunit mENA,
M18647
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                   /product="Na,K-ATPase alpha-1 subunit"
/protein_id="AAA41671.1"
/db_xref="GI:205632"
             GMGAALFMYTHKFTWWFCAFFYSLLIFVYGEVPKLIFFFFFGGWVEKETYY"
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                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
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| 90.7%; Score 3297.4; DB 10; Length 3599; Similarity 98.4%; Pred: No. 0; Length 3599; Similarity 98.4%; Pred: No. 0; Length 3599; Conservative 0; Mismatches 41; Indels 14; GB 50; Conservative 0; Mismatches 41; Indels 14; GB 50; Length 3599; Mismatches 41; Indels 14; GB 50; Length 359; Mismatches 41; Length 3599; Mismatches 41; Length 3599; Mismatches 41; Length 359; Mismat | Qy 963 TG | Oy 903 AG Db 926 AG | Qy 843 TC Db 866 TC | Qy 783 AG Db 806 AG | Qy 723 GAA Db 746 GAA | Qy 663 AA(Db 686 AA(| Qy 603 AGJ Db 626 AGJ | Qy 543 GTT | Qy 483 CCC Db 506 CCC | Oy 423 CCT Db 446 CCT | Oy 363 CGA Db 386 CGA | Qy 303 GAG Db 326 GAG | Qy 243 GAA Db 266 GAA | Oy 183 CCT | Oy 124 CCC | Oy 64 GCA Db 97 GCA | Oy 4 GCC Db 39 GGC | Query Match Best Local Matches 339 | ORIGIN |
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| 99; GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | | CCCC | CAGAATCATATCTGCAAAT CAGAATCATATCTGCAAAT | GGATGTCGTCGTTGGTGAT | CATGGTCCCTCAGCAAGCC CATGGTCCCTCAGCAAGCC | CTGTTTCTCCTATI | ACCACCAAATGATO ACCACCAAATGATO | ACTGTGGATTGGAGCCATT | CCAACTACTCCCGAC CCAACTACTCCGGAC | AACACCGGCAAGGGCCGCT AACACCCGCAAGGCCGGTT | CCATAAACTCAGCCTGGAT CCATAAACTCAGCCTGGAT | CAAGAAGGCGAAGAAG CAAGAAGGCGAAGAAG | gggggttggacgagacaac gggggttggacgagacaac | CTTTCTAGTCTCCAGCCA(CTTTCTAGTCTCCAGCCA | AGTTCCCGCCTCTCGGCT AGTTCCCGCCTCTCGGCT | AGCGGCGGCTCGG | rcggcgggaggaggcggac rcggcgggaggaggcggac | 90.7% imilarity 98.4%; Conservative | 839 a |
| 99; GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG | | GGATTTCACAAACGAGAA GATTTCACAAACGAGAA | GGCTGCAAGGTGGATAA gGCTGCAAGGTGGATAA | CTGGTGGAGGTGAAGGG CTGGTGGAGGTGAAGGG | CTCGTGA | AAGAAGCAAAAAGCT AAGAAGCAAAAAGCT | rgtacctcggggtcgtc gtacctcggggtcgtc | CTITGITTCTTGGC | TCAAATTCTGTCGGCAC CAAATTCTGTCGGCAC | GAGATCCTGGCTCGGGAT gagaTCCTGGCTCGGGAT | AACTCCATCGTAAAT <i>I</i> AACTCCATCGTAAAT <i>I</i> | ACTO ACTO | IATGAGCCCGCAGCTGT TATGAGCCCGCAGCTGT | GCGCGGGGCCG | CCCGGCTCCACTCTCC CCCGGCTCCACTCTCC | 3C-GCTGTCC | CGIGGCAGCGGCGGCG CGIGGCAGCGGCGCG | Score 3297.4; D Pred. No. 0; ; Mismatches | 970 6 |
| | ACT | AA — AA | CTCCTCACTCACTGGTGAA CTCCTCACTCACTGGTGAA | CGGAGACCGAATCCCTGCTG CGGAGACCGAATCCCTGCTG | AGCATCAA AGCATCAA | ATCCTTC | CIGICIGCIGICAIC CIGICIGCIGICGICAIC | CCGAAGTGCTACAG CGAAGTGCTACAG | CTGTTCGGTGGCTTCTC | GGCCCCAACGCCCTCACGC GGCCCCAACGCCCTCACGC | CAGATTTGAGCCGA CAGATTTGAGCCGA | AAGAAGGAAGTGTCTATGG AGAAGGAAGTGTCTATGG | CAGAACATGGGGAC CAGAACATGGGGAC | CGCAGCGCCGCCACCATGG | CAGCCGGGAG-CTGCTCTC CAGCCGGGAGTCTGCTCTC | CTCTTTCCTCCGGCGGCA CTCTTTCCTCCGGCGGCA | GCGGCAGCAGCAGCGGC GCAGCAGCAGCGGC | 10; Length 3599; 1; Indels 14; | |

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ASCICITS-CITSCITTCCENTCCTA-TO-COTOSSANSSSISCASCCCTTASSATGTATCC 3182
                                                                                                                                                                                                                                             CAAACTTSTSAACSASSSICTSATSASSATSASSCTATSAACASATSGGTATGATCAGGC 2822
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                                                                      TTOTTSTOTTOGASSSAASSAASAASAACAASATOTTAATATTTGGCCTCTTTGAAGAGAC 3122
                                                                                                                              CTTTGTCAGTATCGTGGTAGTGAAGAAGAA 3062
                                                                                                                                                                                       SSSSCKSCK STG-PACCT K-SASCKSA-SGAAGATT ITG-PACTT TO CONTROL OF SCCING
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                                                                                                                CTTTGT\AGTATCGTGGCAGAGGAAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (05-JUL-2001) National Institutes of Health, Mammaliar Jene Collection (MGC), Cancer Conomics Office, National Cancer Institute, 31 Center Drive, Prom 11An3, Berhesda, MD 20892-2590,
                                                                                                                                                                                                                                                         Clone distribution: M3C clone distribution information can be for through the I M A G E Consortium/ILINI. at: http://image.llnl.gov. Series: IFAV Plate: if Fow j 70lumn. This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OPF analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement 'Jeffrey Green M.D.
Tissue Procurement 'Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.S.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Eukarycta; Metacoa; Chordata; Craniata; Vertebrata; Euteleestomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   Web site. http://www.hgsc.bcm rmc edu/cdna/
Contact: amg@bcm.tmc.edu
Sunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.
Pichards, S., Gibbs, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project UPL: http://mgc nci nih.gov
Contact. MGC help desk
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/clone="IMAGE:3599053"
/tissue_type="Mammary tumor. C3(1)-Tag model.
/tissue_type="Mammary tumor. C3(1)-Tag model.
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI CGAP_Mam6"
/lab host="PHIOB"
/ncte="Vector: pcMV-SPORT6"
                                                                                                                                                                                                              Location/Qualifiers
1. .3297
                                                                                                                                             /map="FVB/N"
                                                                                                                                                                   /db_xref="taxon:10090"
                                                                                                                                                                                      /organism="Mus musculus"
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Best Local Similarity 95.1%;
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960 CATTGCCTTCTTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACAC 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 CATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACCCCCTCCCACTACTCCCGAATGGGTGAAATTCTGCCGGCAGCTCTTTGGAGGCTTTTC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGITACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTAC 599
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                                                                                                                                                                                                                                                                                           CGCAGAGGATGTCGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCTGC 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAGAACATGGTCCCTCAGCAAGCCCTTGTGATTCGAAATGGAGAGAAATGAGCATCAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGAACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAGAAGATGAGCATCAA 779
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                                                                                                                                                                                                                                           TGCGGAGGATGTCGTCGGGGGATCTGGTGGAGGTGAAAGGGGGAGACCGGATCCCTGC
                                                                                                    ATCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAA
                                                                                                                                      ATCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAA 959
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SAGIKVIMVTGDHPITAKAIAKGVGIISGNETVEDIAARLAII PVNQVNFPDAKACVV
HGSDLKDMTSEELDDIITAYHTEI VFARTSPQÇKLII TUEGCQRQGAI VAVTGORVDSP
ALKKADIGVAMGIVGSDVSKQAADMILLDDNFASI VTGVEEGRLIFDNLKKSIAYTLI
SNIPEI TPFLIF II ANI PLPLGTVTILCIDLGTDMVPAISLAYEQASEDIMKRQPRNP
KTDKLVNERLISMAYGQIGMIQALGGFFTYFVILAENGFLPFHLLGIRETMDDRWVND
VEDSYGQQWTVEQRKIVEFTCHTAFFVSIVVVQWADLVICKTRRNSVFQQGMKNKILI
FGLFEETTALAAFLSYCPGMGAALRMYPLKPTWWFCAFPYSLLIFVYDEVRKLIIRRRP
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QANQENLPILKRAVAGDASESALLKCIEVCCGSVMEMREKYSKIVEIPFNSTNKYQLS
IHKNPNASEPKHLLVMKGAPERILDRCSSILLHGKEQFLDEELKDAFQNAYLELGGLG
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/product="Similar to ATPase, Na+/K+ transporting, alpha
la.1 polypeptide"
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/db_xref="GI-16307541"
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| 2099 1740 | AGGAG DAGGAG | 8 8 |
|--------------|---|----------|
| 2039 1680 | TGCTG | D Q |
| 1979 1620 | ATTTCCC | D 8 |
| 1919 | TAGAGCTGGGGGGCCTTGGAGAGAGCGTGTGCTAGGTTTCTGCCACCTCCTTCTGCC | р Q |
| 1859 | 800 CCTCCTCCACGGCAAGAGCAGCCCCTGGACGAAGAGCTGAAGGACGCCTTTCAGA | 8 8 |
| 1799 1440 | ATGCAGTTCTAT | 유 왕 |
| | TCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGG: | 8 8 |
| 1679 1320 | AGTGGAG AGTGGAG | 8 8 |
| 0 H | TTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGC | 8 8 |
| 1559 1200 | AGAAAACCTGCC | ğ Ş |
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| 1439 1080 | 80 GACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAT | Db VQ |
| 1379 1020 | 20 GGAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCT | Qy Db |
| 1319 960 | 60 GGTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCT | 8 8 |
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A. R. E. Consertium/LLNL. Att. Leaper, and series: IRAL Plate: 7 Row: a Column: 20
Series: IRAL Plate: 7 Row: a Column: 20
This clone was selected for full length sequencing because it This clone was selected for criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC003077 3F80 bg mFNA linear PFI 12 CUL-2001 fonc sapiens, Similar to ATBase, Na+K+ transporting, alpha 1 golypegride, clone MCC13285 1MAGE 2507F85, mFNA, complete cds. BC003077
                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I_M.A G E_Constrtium/LINI_at. http://lmwge.llml.gov
                                                                                                                                                                                                                                                                         cDNA Library Preparation: Rubin Laboratory CENA Library Arrayed by The TM AGE TANGULLA DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project UPL: http://mgc nci nih gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12:PEB:2001) Mattenal Institutes of Health, Mammalian Submitted (12:PEB:2001), Cancer Denomics Office, National Cancer Conne Collection (MCC), Cancer Denomics Office, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3680)
                                                                                                                                                                                                            Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                contact: amadan@systemsbiology.org
Anup Madan, Pachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                           Location/Qualifiers
/organism="Homo sapiens"
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                          .3680
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  TCTCCATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTG
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TGESSEPQTRS PDETFINENPLETENIA FESTNCTUSTARGIVVTTGDRTTWGRIATASG
LEGGQTPIAARIEHFHIITIGVAVFLIGVSFETLISLILEYMLEAVIFLIGIIVANVBE
GLLATUTVCLTLTAKPMARKUCLVKNLBAVETLGSTSTICSDKTGTLTQNPMTVAHM
FDNQIHEADTTENQSGVSFDKTSATWLALSRIAGLCNRAVFQANQENLPILKRAVAGD
ASEAALKCIELCGSVKEMRERYAKTEIPFNSTTMKVQLSILMOPNTSEPQHLLVMK
GAPERILDRGSSILLHGKOPLDESKLVAFONAVELGGERVLGFCHLFLDEDEFP
EGFQFDTDDVNFPIDNLCFVGLISMIDPPRAAVPDAVEKCRSAGIKVLMVTGHHPITA
KAIAKCVGIISEGNETVEDIAARLNIPVSQVNFRDAKACVVIGSDLKOMTSEQLDDIL
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IGMIQALGGFFTYFVILAENGFLPIHLLGLRVDWDDRWINDVBDSYGQQMYYEQRKIV
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/db xref="G1:13111778"
/ctanslation="MGKGVGRDXYEPAAVSEQGDKKGKKGKKDRDMDELKKEVSMDDH
/ctanslation="MGKGVGRDXYEPAAVSEQGDKKGKKDRDMDELKKEVSMDDH
KLSLDELHRKYGTDLSRGLTSARAAEILARDGPNALTPPPTTPEWIKFCRQLFGGFSM
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/tissue type="Brain, neuroblastoma"
/clone_lib="NIH MGC_19"
/lab_host="DH10B-R"
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| 2456 ATSTSTOCAASCAGCTGCISACAISAITCTTCTGGATGACAACTITGCCTCCATOGGA 2515 |
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| (36 F/AFTGFGBAGA) TSCCAGGSSATASCATCSTSGCTCTCACAGGGATGGTGTCA 239 |
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| 2156 COSTOSARACATIOCIOCOCOCTORACATTOCASTGARCEASTGARCECGAGAGATG 2215 |
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| 1916 TGCCTGACGAACASTTTCCCCGAAGSCTTCCAGTTDSACACDSATGAAGTCAATTTCCCCG 1975 |
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| 1796 CTATOCTOCTOCACGACAACGAGCAGCCCTGGACGAGGAGCTGAAGGACGCTTTCAGA 1855 |
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Search completed. March. 6, 2003, 22:59:31 Job time: 9267 secs

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This nuclectide sequence encodes the rat (Na,K)-ATPase alpha 1 subunit (see AAW88390). (Na,K)-ATPase is an ion transporter essential to the cell. The invention provides new, mutated (Na,K)-ATPases (see AAW88287-89) that can be used as novel selectable markers. Appropriate mutation of the (Na,K)-ATPase (see AAW88287-89) that can be used as novel gene (see AAW84294-96) causes a loss in sensitivity of the encoded enzyme to ouabain. A claimed method for detecting transfection or transfecting the cell with a vector carrying a mucleic acid encoding a mutated (Na,K)-ATPase gene of the invention, plus a gene of interest; (b) incubating the cells with a cardioglycoside such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; (c) contacting the incubated cells with a fibringen-coated solid matrix; and (d) detecting any cells bound to the matrix. The new selectable markers are particularly useful where antibiotic
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| 1860 | CTCCTCCACGGCAAGGAGCAGCCCCTGGACGAAGAGCTGAAGGAACGCCTTTCAGAATGCC | 1801 | 99 |
|--------------|--|--------------|----------|
| 1800 | AAGCACCTGCTAGTGATGAAGGGCGCCCAGAAAGGATCCTGGACCGATGCAGTTCTATC | 1741 1741 | Db Qy |
| 74 | AGTACCAGCTCTCCATTCACAAGAACCCA | | Db. |
| 1680 | TCTGCTGTGGCTCCGTGATGGAGGAGTACGAGAGATACACCAAGATAGTGGAGATTCC TCAACTCCACCAACAAGAGTACCAGCTCTCCGTTCAGAAGAACCCAAAAGATAGGAGATTCC | 1621 | S B |
| 20 0 | GTGGCTCCGTGATGAGAGATSAGGGAGAAGTACACCAAGATAGTGGAGATTCC | 6 | . S |
| 1620 | ATCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAG | 1561 | מם |
| 1620 | TCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGA | 1561 | γQ |
| 1560 1560 | TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTGCCT | 1501 | 9g V2 |
| 1500 | .CCACAGAGAATCAGACTGGGGGGTCTCCTTTJACAAGACGTCAGCCACCTGGTTCGGTCT | 1441 | ДĎ |
| 1500 | ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCAGC | 1441 | γQ |
| 1440 | ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGAC | | DЬ |
| 1440 | CTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGA | 1381 | Qy |
| 1380 | GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG | 1321 | Db |
| 1380 | AAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCT | 1321 | Qy |
| 1320 | GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGTAACTGCCTGGTGAAGAACCTG | 1261 | Дb |
| 1320 | TATUTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACC | 1261 | γQ |
| 1260 | CAC | 1201 | Дb |
| 1260 | TCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCA | 1201 | γQ |
| 1200 | CIGGGGGIGTCTTTCTTCATTCTCTCTCTGATCCTTGAGTACACCTGGCTCGAAGGCTGTC | 1141 | Дb |
| 1200 | TGGGGGTGTCTTCTTCTCTCTCTGTGATCCTTGAGTACACCTGGCTCGAGGCTGT | 1141 | γQ |
| 1140 | ACCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGTGTGGCCGTGTTC | 0 | DЬ |
| 1140 | .CCCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTT | 1081 | Ş |
| 0 | | Ö | dd dd |
| 1080 | GGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTG | | 0 |
| 1020 | ATTGCCTTCTCTAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACT | | Db |
| 1020 | TTGCCTTCTTCTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACA | | γQ |
| 960 | TCAGAACCCCAGACTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAAC | 901 | DЪ |
| 960 | CAGAACCCCAGACTCGGGTCCCCGGATTTCACAAACGAGAACCCCCTTGGAGACAAACGA | 901 | γ0 |
| 0 | AG - | 841 | 90 |
| 900 | TESSTO V O TO VIOLO DE VIOLENTA VENTERE V VENTO SE VIOLO VIOLVA VIOLO VI | 841 | ? |
| 4 | D : | | Db . |
| 4 | CAGAGGATGTCGTCGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCTGC | 781 | 5 |
| 780 | AGGACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAATGAGAAGAAGAAGAACATCAAC | 721 | Дb |

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                                                                                                                                                                           Rat; ss; (Na,K)-ATPase; 799/801NKA; mutant; ouabain; gene therapy.
                                                                                                                                                                                                        Rat cDNA encoding partial wild-type (Na, K)-ATPase.
                                                                                                                                                                                                                                        14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                  AAS16480 standard; cDNA; 3636 BP
                                                                                                                                                  Rattus rattus.
                            sig_peptide
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                                           /*tag= a/product= "(Na,K)_ATPase_799/801NKA"/product= "(Na,K)_ATPase_799/801NKA"/partial/note= "No start or stop codon"/
 /*tag= b
/label= Start_peptide
                                                                                                                   Location/Qualifiers
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Matches 3633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid encoding an ouabain-resistant (Na,K)-ATPase termed 799/801NKA, a vector comprising the nucleic acid and a cell comprising the vector. The nucleic acid is useful as a selective marker to screen for transformed cells in gene therapy. Unlike prior art selective markers, the gene is already expressed in all mammalian cells and the minor mutation is more natural than adding an artificial gene or making major mutations so the invention is more sultable for selecting cells for transplantation into a patient. The present sequence encodes wild-type rat (Na,K)-ATPase protein used as the basis for the mutated proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding an ouabain-resistant (Na,K)-ATPase for use as a selectable marker for transformed mammalian cells, particularly suitable when selecting cells for transplant into a patient -
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                                                                                                                                                                                                                                          GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG
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                                                                                                      ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTG 1500
                                                                                                                                                                  ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGAC 1440
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| 221 GCCTGTGTAGTACATGGCAGTGACTTGAAGGACATGACCTCTGAGGAGCTGGATGACATT 228 | Db |
| 221 GCCTGTGTAGTACATGGCAGTGACTTGAAGGACATGACCTCTGAGGAGGTGAATGACATT 228 | Ş |
| 161 GAAGACATTGCTGCCCGCCTCAACATTCCAGTGAACCAGGTGAACCCCAGAGATGCCAAG 222 | фd |
| 61 GAAGACATTGCTGCCCGCCTCAACATTCCAGTGAACCAGGTGAACCCCAGAGATGCCAAG 222 | γQ |
| [01 ATEACAGECAAAGECATTGCTAAGGGGGTGGGCATTATCTCAGAAGGTAACGAGACCGTG 21 | Дb |
| 01 ATCACAGCCAAAGCCATTGCTAAGGGGGTGGGCATTATCTCAGAAGGTAACGAGACCGTG 21 | γ |
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| 41 GCTGTG9GGAAATGCCGCAGGGCTGGGATTAAGGTCATCATGGTCACAGGAGACCATCCA 210 | , 9 |
| 81 AACCTCTGCTTCGTGGGTCTTATCTCCATGATTGACCCTCCTCGAGCTGCTGTCCCCGAT 20 | dd |
| 81 AACCTCTGCTTCGTGGGTCTTATC | γΩ |
| 21 GACGAACAGTTTCCCGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCCCCGTGGA | ДЪ |
| 21 GACGAACAGTTTCCCGGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCCCGTGGAT 198 | Qy |
| 61 TACCTAGAGCTGGGGGGCCTTGGAGAGCGTGTGCTAGGTTTCTGCCACCTCCTTCTGCC | дb |
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| 1 AAGCACCTGCTAGTGATGAAGGGCGCCCCAGAAAGGATCCTGGACCGA | Q V |
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| GAGATTCC | dd Yy |
| 561 AICCIIANGCGIGCAGARATGGAGAGAGAGAGAGAGAGAGAGATAGIGGAGATTCCC 16 |) D |
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| 3601 GGATTTTACAAATAAAGATGGCTATTATAA | GGATTTTACAAATAAAGATGGCTATTATAA | CCTTTTTGTTTTGTAAAAAAGGAAAACCT | 3541 CCTTTTGTTTTTGTAAAAAAGGAAAACCT | 3481 GGGGAGGGCTGCCCGAAAAACA | 34 | 3421 CCAAAGCATGTGGGGATCCAGA | QY 3421 CCAAAGCATGTGGGGATCCAGACGTCCTGGAATGAAGC | 3361 TACCCCCCTTTGTGTACTT | 3361 TACCCCCCCTTTGTGTACTT | 301 TACTACTAGCCACTGCCCT | 330 | 3241 GACGAGGTG | w | 3181 CCCCTCAAA | 318 | 3121 ACAGCTCTT | ACAGCTCTTGCTGCTTTCCTGTCCTACTGCC | 3061 AATTCTGTCTTC | w | 3001 TTCTTTGTCAGT | 3001 TTCTTTG | 2941 TACGGGCAGCAGTGGACCTACGAGCAG | 2941 TACGGGCAGCAGTGGACCTACGAGCAGAGGA | 2881 CACCTGTTGGGCATCCGAGAGACCTGGGATGA | 2881 CAC | 2821 GCC | 282 | 2761 GAC | 27 | 2701 CTG | 2701 CTGGCCTATGAACAGGCTGAAAGTGACATCA | |
| GGA | CGGAA 3636 | SACTGAAAGATTACGTTTTATATC | Ó | GCGGGGAAGGTTTATATGTG 354 | GCGGGAAGGTTTATATGTG 354 | ATGTAGCTGTAATGGGGGGGGGG | ATGTAGCTGTAATGGGGGGCGG | ACTCTACCCTGGTAGGAAAGCA 342 | . 4 | TGTGCCACACTGCACCTACCCC 336 | TGTGCCACACACTGCACCTACCCC 336 | GGCGGCTGGGTGGAGAAGGAAACC 330 | CCTGGCGGCTGGGTGGAGAAGGAAACC 330 | CTTCGTGTAT 324 | CTTCGTGTAT 324 | raggargrat 318 | 1 8 | CTCTTTGAAGAG 312 | CTCTTTGAAGAG 312 | AAGACCAGAAGG 306 | TGGTCATCTGCAAGACCAGAAGG | trigrégaerreacereceacacesce 300 | ATTGTGGAGTTCACCTGCCACACGGCC 300 | ĆĠĊŦĠĠAŦĊAATĠATĠŦĠĠĀĠĠĀĊĀĠĊ 2 | GACAGC 294 | CCCTTT 288 | CCCTTT 288 | CGGTATGATCCAG 28 | CGGTATGATCCAG 282 | AAATCCCAAAACG 276 | 76 | GCCATCTCT 27 |

RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                     ruration, Arained by mutageness of the (Na,K)-AIPse gene (see AAV84297), causes a loss in sensitivity of the encoded enzyme to cushain. A claimed method for detecting transfection or transformation of a sukary-discall congrises: (a) transformation of a sukary-discall congrises: (a) transformation of a sukary-discall congrises: (a) transformation of the cell with a vertor carrying a nucleic acid encoding a mutated (Na,K)-AIPse gene of the invention, plus a gene of interest, in) incubating the cells with a cardically-coside such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; (c) contaging the incubated cells with a fittingen-costed solid matrix; and (d) detecting any cells bound to the matrix. The new selectable marker is particularly useful where antibiotic resistance selection is undesirable, e.g. in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This nuclearide sequence encodes a new mutated (Na,K)-Ampase alpha subunit (see AAW8825), in which the Leu-879 residue of the native rat projein (see AAW8425), has been mutated to systeine. This mutated projein can be used as a novel selectable marker. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                               Sequence 3636 BP; 850 A; 967 C; 995 G; 824 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 45 49; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mutated (Na, K) -ATPase - useful as a selection marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Selectable marker, (Ma,K)-Arrase, rat, gene therapy, mutant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUN 1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HARO ) MARCHINERA INMOVATIONS AB.
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                                                                                                                                             CAGCCTASTTOCOSCUTCTOSSCTOCOCOSCTOCACTCTOCCASCOSGAGCTSCTCT
                                          | GGGAAGGGGGTTGGACGAAGTATGAGCCCGCAGAGTTGTATCAGAACATGGGGACAAG 300
                                                                                                                                                                                                     1999-059908/05
                             GGGAAGGGTTGGACATGACAACAACTATGAGCCCGCAGCTGTATCAGAACATGGGGACAAG
                                                                                     97SE-0002120.
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| ζy | Qу | Db Qy | Qy | B S | Qy | ₽ Q | 9d 75 | Db Sy | B 8 | 동양 | 무작 | 용 왕 | B & | 4 VQ | dg dd | 8 8 | B & | Ðά |
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| 1381 | 1321 1321 | 1261 1261 | 1201 1201 | 1141 1141 | 1081 1081 | 1021 | 961 961 | 106 105 | 841 841 | 781 781 | 721 721 | 661 661 | | 541 541 | 4 t l 4 t l | 421 421 | 361 | 301 |
| ACTORGRACOGURTGACAGTGACTACATGTGGTTGACAATGAAATGGATGAGGTGAG | GAAGCISTGJAGACCTTYJGFTYYACATYCACCATCTYGTTYYGACAAGACTGGAACTCTG | GTATGTCIGACSCTCACTGCCAAGCSCATSSCSAASAAGAACTGCCTGSTGAAGAACCTG 1 | ATCTTCUTCATTGGTATCATCGTAGCCAACGTGCCGAAGGTTTGGTGGCCACGGTCAGG | CTGGGGGTFCTTTCTTCATTCTCTCTCTGATCCTTGAGTACACCTGGCTTGAGGCTGTC 1 | ACCCCCATTGCTGAAGAAATCGAGCACTTCATCACCTCATCACGAGGGGTGTGGGTGTTC 1 | GRANATOGEACOGIANTRAGRACARSANOSCEACOGITECTTOTRAGRACTRAAACACGRACTS | ATTGCCTTCTTCTCAACCAACTSTGTTSAASSAACTSCATGTGSTATCGTTTGTGTACACT | TCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAACG | GATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTGGTGAA G | GCAGAGGATGTCGTCGTTGGTGATCTGGTGAAGGGGGAAGACCGAATCCCTGCT 8 | AASAACATSSTOOTTOASCAASCCTOSTSATTOSAATSSASAGAAGATSAGCATCAAC 7 | ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC 7 | GANGAGGAACCACCAAATGATGATCTSTACCTCGGGGGGGGGTGCTGTCTGCTGTCGTCATC 6 | ATGITACIGIGSAITGSASCCAITCITIGITTCTPSTTTATGS-AFCCGAAGTGCTACA 6 | COCCETOCCACTACTCCCGAGTGGGTCAAATTCTGTCGGCAGCTGTTCGGTCGG | GROCTAACACHARAAGACCSCTSAGATACTSAGT-SSAATSACACACACTCAAGG | CCATAAACTCAGCCTGSATGAACTCCATCGTAAATACGGAAAAAATTTTGAGTGA | ANGAGAKANAGCANAGAASAASAASAGAAATAGAACTCAAGAAGAAGTATCAAGAAGAAGTATCAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG |
| 440 | 380 380 | 320 320 | 250 250 | 200 | 140 140 | 0 8 C | 020 | 60 60 | 0 0 0 | 40 | 90 | 20 | 60 | 2 2 | 40 | 8 9 | | 2 |

| TCCAAGCAAGCTGCTSACATGATTCTTCTGGATGACAACTTTGCCTCCATCGTGA | Oy Db |
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| TCTCCAGCTTTGAAAAAGGCAGATATTGGGGTTGCCATGGGGATTGTTGGCTCGGATGTG 24 | dd VQ |
| GTGGAGGGTGCCAGGGTGCCATCGTGGCTGTCACAGGGATGGTGTCAATGAC 240 | |
| TIGGGGTACCACACGAGATIGICIIIGCIAGGACCTCICCIACACACGAGCCCATCATT TTGCGGTACCACACGAGATTGTCTTTGCTAGGACCTCTCCTCAACAGAAGCTCATCATT 234 | |
| GCCTGTGTAGTNCATGGCAGTGACTTGAAGGACATGACCTCTGAAGGAGCTGGATGACATT 228 | |
| GANGACATTGCTGCCCGCCTLAACATTCCAGTGAACCAGAGATACCCCAGAGATGCCAAGATGCAAGATGCAAGATGCCAAGATGCCAAGATGCCAAGATGCCAAGATGCCAAGATGCCAAGATGCCAAGACCCAGAGAACCCCAGAGATGCCAAGACCAGTGAACACCCCAGAGATGCCAAGACCAGTGAACACTCCAGTGAACCAGTGAACCAGTGAACAATT 228 | |
| TCACAGCCAAAGCCATTGCTAAGGGGTGGGCATTATCTCAGAAGGTAACGAGACGTG 21 | DP Võ |
| GCTGTGGGCAAATGCCGCAGCGCTGGGATTAAGGTCATCATGGTCACAGGACACCATCCA 210 | |
| AACCTCTGCTTCGTGGGTCTTATCTCCATGATTGACCCTCCTCGAGCTGCTGTCCCCGAT 20 | |
| GACGAACAGTTTCCCGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCCCGTGGAT 198 | |
| TACCTAGAGCTGGGGGGGCCTTGGAGAGCGTGTGCTAGGTTTCTGCCACCTCCTTCTGCCT 192 | |
| TTCCTCCACGGCAAGGAGCAGCCCCTGGACGAAGAGCTGAAGGACGCCTTTCAGAATGCC 1 | |
| AGCACCTGCTAGTGATGAAGGGCGCCCAGAAAGGATCCTGGACCGATGCAGTTCTATC 180 | |
| TTCAACTCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGGAGCCT 17 | |
| TROTGCTGTGGCTCCGTGATGGAGATGAGGGAGAAGTACACCAAGATAGTGGAGATTCCC 168 | |
| TCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAG 162 | |
| CCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTGCCT 15 | Qy Db |
| CCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTGGCTCTG 15 | |
| ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGAC 14 | DЬ |

| 3541 CCTTTTGTTTTIGTAAAAAAGGAAAACCTGGAAAGACTGAAAGATTACGTTTTATATCT 3600 | Qy db |
|---|---------------|
| 81 GGGGAGGGCTGCCCGAAAAACACCGTGGACGGGGACGACGACGGGGAAGGTTTATATGTTG 35 | D Qy |
| 421 CCAAAGCATGTGGGGATCCAGACGTCCTGGAATGAAGCATGTAGCTGTAATGGGGGGCGG 348 | Qy db |
| TACCCCCCTTTGTGTACTICAAGTCTTGGAGCTCGGAACTCTACCCTGGTAGGAAAGCA 342 | Qу |
| TACTACTAGCCCACTGCCCTGCACGCCGTGGAACATTGTGCCACACACTGCACCTACCCC 336 | Qy Db |
| GACGAGGTGCGGAAGCTCATCATCAGGCGACGCCCTGGCGGCTGGGTGGAGAAGCAAACC 330 | dg VQ |
| CCCCTCAAACCTACTTGGTGGTTCTGTGCCCTTCCCCTACTCCCCTTCTCATCTTCGTGTAT 324 | Qy Db |
| ACAGCTCTTGCTGCTTTCCTGTCCTACTGCCCTGGGATGGGTGCAGCCCTTAGGATGTAT 318 | g 64 |
| AATTCTGTCTTCCAGCAGGGAATGAAGAACAAGATCTTAATATTTGGCCTCTTTGAAGAG 312 | Qy Db |
| TTCTTTGTCAGTATCGTGGTAGTGCAGTGGGCTGACTTGGTCATCTGCAAGACCAGAAGG 306 | d do |
| TACGGGCAGCAGTGGACCTACGAGCAGAGGAAGATTGTGGAGTTCACCTGCCACACGGCC 30 | Qy dg |
| CACCTGTTGGGCATCCGAGAGACCTGGGATGACCGCTGGATTAATGATGTGGGGGACAGC 294 | Db Oy |
| TTCTTCACTTATTTTGTGATTCTGGCTGAGAACGGTTTCCTGCCCTTT 288 | 9 79 79 |
| GACAAACTTGTGAACGAGCGTCTGATCAGCATGGCCTATGGACAGATCGGTATGATCCAG 282 | D Qy |
| CTGGCCTATGAACAGGCTGAAAGIGACATCATGAAGAGGCAGCCCAGAAATCCCAAAACG 27 | 9d 4d |
| CTGGGCACCGTGACCATCCTCTGCATTGACTTGGSCACTGACATGGTTCCCGCCATCTCT 270 | D Qy |
| AGTAACATTCCGGAAATCACCCCCTTCTTGATATTTATTGCTAACATTCCACTGCCC 264 | Db dd |
| TTAGAAGAAGGTCGTCTGATATTTGATAACTTGAAGAAATCCATTGCTTACACCCCTAACA 258 | Qy |

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                                                                                                                                                                                                                                transformation of a eukaryotic cell comprises: (a) transforming or transfecting the cell with a vector carrying a nucleic acid encoding a mutated (Na,K)-ATPase gene of the invention, plus a gene of interest; (b) incubating the cells with a cardioglycoside such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; as digitoxin in the incubated cells with a fibringen-coated solid matrix; and (d) detecting any cells bound to the matrix. The new selectable marker is particularly useful where antibiotic resistance selection is undesirable, e.g. in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                           This nucleonide sequence encodes a new mutated (Na,K)-ATPase alpha 1 subunit (see AAW88299) in which the Leu-881 residue of the native rat protein (see AAW88299) has been mutated to cysteine. This mutated protein can be used as a novel selectable marker. The
                                                                                                                                                                                                                                                                                                                                                                 mutation, obtained by mutagenesis of the (Na,K)-ATPase gene (see AAV84297), causes a loss in sensitivity of the encoded enzyme to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-059908/05.
P-PSDB; AAW88288.
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| CCC DAACOORTEGETTGCCCTTCTTCTTCTTTTTTTTTTTTTTTTTTTT | |
| O1 ATCACAGCCAAAGCCATTGCTAAGGGGGTGGGCATTATCTAGAAGGTAACGAAGGCGTG 21 | |
|)41 GCTGTGGGCAAATGCCGCAGCGCTGGGATTAAGGTCATGATGGTCACAGGAGACCATCCA 210 | |
| 941 GCTGTGGGCAAATGCCGCAGCGCTGGGATTAAGGTCATCATCGTCACAGGAGACCATCCA 2 | |
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| 21 GACSAACAGTTTCCCGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCCCGTGGAT 198 | |
| 21 GACGAACAGTTTTCCCGAAGGCTTCCAGTTTTGACGATGAAGTCAATTTTCCCCGTGGAT 198 | |
| 61 TACCTAGAGCTGGGGGGCCTTGGAGAGCGTGTGCTAGGTTTCTGCCACCTCCTTCTGCCT | |
| 61 TACCTAGAGCTGGGGGGCCTTGGAAGAGCGTGTGCTAGGTTTCTGCCACCTCCTTCTGCCT 19 | |
| 01 CTCCTCCACGGCAAGAAGAGCCCCTGGACGAAGAGCTGAAGGACGCCTTTCAGAATGCC 18 | Db . |
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| 81 TTCAACTCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGGAGCCT 174 | |
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| 1 CCAAAGCATGTGGGGATCCAGACGTCCTGGAATGAAGCATGTAGCTGTAATGGGGGGCGG 3480 | ACCCCCCTTTGTGTACTTCAAGTCTTGGAGCTCGGAACTCTACCCTGGTAGGAAAGCA 342 | TACCCCCCCTTTGTGTACTTCAAGTCTTGGAGCTCGGAACTCTACCCTGGTAGGAAAGCA 342 | TACTACTAGCCCACTGCCCTGCACGCCGTGGAACATTGTGCCACACACTGCACCTACCCC 336 TACTACTAGCCCACTGCCCTGCACGCCGTGGAACATTGTGCCACACACA | GACGAGGTGCGGAAGCTCATCAGCGACGCCCTGGCGGCTGGAGGAGAAGGAAACC 33 | GACGAGGTGCGGAAGCTCATCATCAGGCGACGCCCTGGCGGCTGGGTGGAGAAGGAAAACC 330 | CCCCTCAAACCTAC 116916911C1991C119CC11CCCTCACTCCCTCAAACCTACTTCGTGTAT 324 | CAGCICITECIECIA COMPONENTA CONTROLO CON | ACAGCTCTTGCTGCTTTCCTGTCCTACTGCCCTGGGATGGTGCAGCCCTTAGGATGTAT 3180 | | TCTGTCTTCCAGCAGGAATGAAGAACAAGATCTTAATATTTTGGCCTCTTTGAAG | TTCTTTGTCAGTATCGTGGTAGTGCAGTGGGCTGACTTGGTCATCTGCAAGACCAGAAGG 3060 | cggcagcagtagtacctacgagcagaggaagattgtggagttcacctgccacacggcc 300 | 300 GCAGCAGTGGACCTACGAGCAGAAGGAAGATTGTGGAGTTCACCTGCCACACGGCC | CACCTGTTGGGCATCCGAGAGACCTGGGATGACCGCTGGATTAATGATGTGGACGACGGC 2940 | TTCCTGCCCTTT 288 | CTGGGAGGCTTCTTCACTTATTTTGTGATTCTGGCTGAGAACGGTTTCCTGCCCTT | GACAAACTTGTGAACGAGCGTCTGATCAGCATGGCCTATGGACAGATCGGTATGATCCAG 2820 | TGAAAGTGACATCATGAAGAGGCAGCCCAGAAATCCCAAAACG 276 | TGGCCTA | 0 0 | GTAACATTCCGGAAATCACCCCCTTCTTGATATTTATTATTGCAAACATTCLACIGLCC | 0 0 | CATTGCTTACACCCTAACA 2 | TAGAAGAAGGTCGTCTGATATTTGATAACTTC | CCTCCATCGTGAS | CCAAGCAAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTTCCATCGTGACTGG | | CTCCAGCTTTGAAAAAGGCAGATATTGGGGTTGCCATGGGGATTGTTGGCTCGGATG | |

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                                                                                                                        New nucleic acid encoding an ouabain-resistant (Na,K)-ATPase for use a selectable marker for transformed mammalian cells, particularly suitable when selecting cells for transplant into a patient \, -
                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat; ss; (Na,K) ATPase, 799/901NKA, mutant, ouabain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat cDNA encoding partial (Na,K)-ATPase mutant 799/801NKA
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         prior are selective markers, the gene is already expressed in all mammalian cells and the minor mutation is more natural than adding an
                                                                                               Disclosure; Column 38-40; 30pp; English.
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artificial gene or making major mutations so the invention
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241..3636
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replace_'(2635,T)
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/product= "(Na,K)_ATPase_700/R01NKA"
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                       GCASA93ATGTCGTCGTTGGTGATCTGGTGJAGGGTGAAGGGGGGAAGGGGGAATCCCTGCT
                                                                                                                                                                                                                                            GACGACCATAAACTCAGCCTGGATGAACTCCATCGTAAATACGGAACAGATTTTGAGCCGA
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                                                                       GCAGAGUÁTGT CETT GETT GETT GÁT CT GETT GA GETT GA Á GEG GET GA GA COGA TOCCT GOT
                                                                                                                                                                        ATAACTSGCTGTTTCTCCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATSGAATCCTTC
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                                                                                                                                                ANGANCATEGTCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAGAAGATGAGCATCAAC
                                                                                                                                                                                                                         ATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTACA 600
                                                                                                                                                                                                                                                                                                  ATGITACTGTGGATTGGAGCCATTCTTTGTTTGTTTGGCTTATGGCATCCGAAGTGCTACA 600
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Pred. No. 0;
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| 921 GACGAACAGTTTCCCGGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCCCCGTGGAT 198 | D) |
| GAACAGTTTCCCGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCCCGTGGAT 198 | 9 |
| Y 1861 TACCTAGAGCTGGGGGGCCTTGGAAGACCTGTGCTAGGTTTCTGCCACCTCCTTCTGCCT 1920 | B 8 |
| 1801 CTCCTCCACGGCAAGGAGCAGCCCCTGGACGAAGAGCTGAAGGACGCCTTTCAGAATGCC 186 | B 8 |
| 1741 AAGCACCTGCTAGTGATGAAGGGCGCCCAGAAAGGATCCTGGACCGATGCAGTTCTATC 180 | B 8 |
| 1681 TTCAACTCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGGAGCCT 174 | 40 |
| 1621 GTCTGCTGTGGCTCCGTGATGGAGGAGATGAGGGAGAAGTACACCAAGATAGTGGAGATTCCC 1 | £ 8 |
| - ب | d dd |
| y 1501 TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACAAGAAAACCTGCCT 1560 | D QY |
| y 1441 ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTG 1500 | 8 8 |
| 1381 ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGAC 1440 | g & |
| , 1321 GAAGCTGTGGAGACCTTYXGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG 1380 | B & |
| , 1261 GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCTG 1320 | g 8 |
| 1201 ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCACG 1260 | 90 80 |
| , 1141 CTGGGGGTGTCTTTCTTCATTCTCTCTGATCCTTGAGTACACCTGGCTCGAGGCTGTC 1200 | B & |
| 1081 ACCCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGGCGTGTTC 1140 | D Ç V |
| 1021 GAGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCCTG 1080 | 90 |
| 961 ATTGCCTTCTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACT 1020 | 8 |
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| 41 GCTGTGGGCAAA 1 | |
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| 041 | DЬ |
| CCATTECTAAGGCGTGGGATTAÄĞĞTCÄTÖĞTCÄCÄĞĞ | 1981 AACCTCTGCTTCGTGGGTCTTATCTCCATGATTGACCCTCCTCGAGCTGCT 2041 GCTGTGGGCAAATGCCGCAGCGCTGGGATTAAGGTCATCATGGTCACAGGA |
| SACCATCO SAGACCATCO SAGACCATCO SAGACCATCO SAGACCATCO SATTOCAM SATT | 10 |

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04-JUN-1998;
                                                                                          mat_peptide
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                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                             AAS16478 standard; cDNA; 3636 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACCCCCCCTTTSTSTACTTCAASTCTTGSAGCTCSSAACTCTACCCTGSTASGAAAASCA 3420
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                                                                                                                                                                                                                                                                                                                                            GGATTTTTACAAATAAACATGGCIATTATAACGGAA 3636
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
98US-0090535
                                                                                                                                                                                                                     ATPase, 799/8013KA; mutant, buabain, gene therapy
                                                            replace (2641, C)
                                                                                         /label= Start_peptide
241..3636
                                                                                                                                             /**ag= a
/product= "(Na,K)_ATPase_799/801NKA"
                                                                     /label= Mature_(Na,K)_ATPase_799/801NKA
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                                                                                                                              /note= "No start or stop codon'
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P-PSDB; AAU10499.
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ATGITACIGIGGATTGGAGCCATTCTTTSTITCTFGGCTTAT5GCATCCGAAGTGCTACA
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                                                                                                                                                                                                                                                                                                                                                                            GACGACCATAAACTCAGCCTGGATGAACTCGATCGTAAATACGGAAATAGATTTGAGCCGA
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| GTCTGCTGTGGCTCCGTGATGGAGATGAGGGAGAAGTACACCAAGATAGTGGAGATTCCC | ATCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAG 1620 | TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAGAAAACCTGCCT 1560 | ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTG 1500 | ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCCATGATGAAGCTGAC 1440 | GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG 1380 | GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCTG 1320 | ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGAAGGTTTGCTGGCCACCGTCACG 1260 | CTGGGGGTGTCTTTCTTCATTCTCTCTCTGATCCTTGAGTACACCTGGCTCGAGGCTGTC 1200 | ACCCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTTC 1140 | GGGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCCTG 1080 | ATTGCCTTCTTCTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACT 1020 | TCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAAC 960 | GATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTCA | GCAGAGGATGTCGTCGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCCTGCT 840 | AAGAACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAGAGA | ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC 720 | BAAGAGGAACCACCAAATGATGATCTGTACCTCGGGGTCGTGCTGTCTGCTGTCGTCATC 660 | NTGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATG3CATCCGAAGTGCTACA 600 |

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            Sclostable marker,
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                                                                                                                 AAV84296 standard;
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                                                                                                                                                                                                                                                                                                                                     SCCTISSIASSCITCTICACTIATTTSTSATTCTSSCISASAACGSTTTCCTGCCTTT
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                                                                                                                                                                                                                                                                                                     GRRGARRESTROCCOGAAAAACACCSTROGGOGGGACAGCGGGGGAAGAGTTTATATGTG
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                                   ATPase alpha 1 subunit (Lk740, L0810, mutant)
                                                             (first entry)
                                                                                                                                                                                                                                                                                      `TGCCCGAAAAACACCGTGGACGGGGACGACAGCGGGGGAAGGTTTATATGTG
            (Na, F) ATFase,
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transformation of a eukaryotic cell comprises: (a) transforming or transfecting the cell with a vector carrying a nucleic and encoding a mutated (Na,K). ATPase gene of the invention, plus a gene of interest; (b) incubating the cells with a cardingly-neide such as digitoxin, digitogenin, digoxin, bufalin or (especially) ouabain; (c) contacting the incubated cells with a fibring-n-coated solid matrix; and (d) detecting any cells bound to the matrix. The new
                                                                                                                                                                                                  This nuclectide sequence encodes a new mutated (Na,K) ATPase alpha I subunit (see AAW88288), in which the Leu-879 and Leu-881 residues the native rat protein (see AAW88290) have been mutated to cysteine. This mutated protein can be used as a novel selectable marker. The mutation, obtained by mutagenesis of the (Na,K) ATPase gene (see AAV84297), causes a loss in sensitivity of the encoded enzyme to causain. A claimed method for detecting transfertion or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Belusa R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pattus rattus.
Synthetic.
                               selectable marker is particularly useful where antihictic resistance selection is undesirable, e.g. in gene therapy.
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 54-58; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             New mutated (Na, K)-ATPase - useful as a selection marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KARO-) KAROLINSKA INNOVATIONS AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-1997;
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Of

Sequence 3636 BP; 850 A; 966 C; 995 G; 825 T; 0 other;

Query Match

Local

Similarity

99.6%; Score 3621.6;

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| ACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTG 1 | _ |
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| ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAAATCAAATCCATGAAGCTGAC 144 | DЬ |
| ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGAC 1 | |
| GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG | |
| GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG 13 | |
| GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAACAACTGCCTGGTGAAGAACCTG 13 | |
| GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCTG 132 | |
| ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCACG 12 | |
| ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCACG 126 | |
| CTGGGGGTGTCTTTCTTCATTCTCTCTCTGATCCTTG | |
| ACCCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTTC 114 | |
| ACCCCCATTGCTGAAGAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTTC 1 | |
| GGGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCCAG 10 | |
| GGGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCCTG 108 | |
| ATTGCCTTCTTCCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACT 10 | |
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| GATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTCA | |
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| GCAGAGGATGTCGTCGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCCTGCT 84 | |
| 721 AAGAACATGGTECCTCAGCAAGGCCTCGTGATTCGAAATGGAGAGAAGATGAGCATCAAC 780 721 AAGAACATGGTECCTCAGCAAGGCCTCGTGATTCGAAATGGAGAAGATGAGCATCAAC 780 721 AAGAACATGGTECCTCAGCAAGGCCTCGTGATTCGAAATGGAGAAGAAGATGAGCATCAAC 780 | dg VQ |
| ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC 72 | |
| ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAAGCTCCAAGATCATGGAATC | |
| GAAGAGGAACCACCAAATGATGATCTGTACCTCGGGGTCGTGCTGCTGCTGCTGTCGT | |
| GAAGAGGAACCACCAAATGATGATCTGTACCTCGGGGTCGTGCTGTCTGCTGTCGTCATC 6 | |
| ATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTACA 6 | |
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| CCCCCTCCACTACTCCCSAGTGGGTCAAATTCTGTCGGCAGCTGTTCGGTGGCTTCTCC 54 | g & |
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| AGTAAC | GTAGAA(GTAGAA(| TCCAAGO TCCAAGO | TCTCCAG | GIGGAGG GIGGAGG | TTGCGGT | GCCTGTG GCCTGTG | GAAGACA GAAGACA | ATCACAG | GCTGTGG GCTGTGG | AACCTCT AACCTCT | GACGAAC GACGAAC | TACCTAG | CICCICC | AAGCACC AAGCACC | TTCAACT | GTCTGCT | ATCCTTAA ATCCTTAA | CCAGAA |
| AACATTCCGG | GAAGGTC | CAAGCTG | CTTT | GCTGCCA | ACCA ACCA | TAGTAC | TTGCTG | CCAAAGC | GCAAATG GCAAATG | GCTTCG1 | AGTTTCC | AGCTGGG AGCTGGG | ACGGCAA ACGGCAA | TGCTAGT | CCACCAA | GIGGCIC | GCGTGC GCGTGC | TIGCTGGT |
| HAAATCAC | GTCTGAT | CTGACATO | SAAAAAGGC SAAAAAGGC | AGCGGCAGGGT AGCGGCAGGGT | ନ୍ଦ୍ର-ନ | ATGGCAGT | CCCGCCT | CATTGC | CCGCAG | GGGTCTT | CGAAGG CGAAGG | GGGCCTT | GGAGCAG | TGATGAAG TGATGAAG | CAAGTAC | CGTGATO | AGTAGCG | |
| CCCCCTTC | ATTTGAT | GATTCTT | AGATATT | GGGIGCC | 걸=걸 | GACTIG | CAACATT CAACATT | TAAGGGGG } TAAGGGGG | CGCTGGG | ATCTCC | CTTCCAG CTTCCAG | GGAGAG GGAGAG | CCCCIG | 990900 | CAGCTC | GGAGATGA GGAGATGA | GGAGATG | |
| TTGATA | AACTTG AACTTG | CTGGATG | GGGGTT GGGGTT | ATCGTG | GCTAGG GCTAGG | AAGG | CCAGTGA | GTGGGCA GTGGGCA | ATTAAGG | ATGATTG | TTTGACA | CGIGIGC CGIGIGC | GACGAAG GACGAAG | CCAGAAA CCAGAAA | TCCATTC TCCATTC | GGGAGA GGGAGA | CTTCCG | CAGTGT |
| TTTATTA | AAGAAAT AAGAAAT | SACAACTT SACAACTT | GCCATGGG | 01010 | CCTCTC | TGACCT | AACCAGG AACCAGG | TTATCT | TCATCAT | ACCCTCC | CTGATGA CTGATGA | TAGGTTT TAGGTTT | AGCTGAA AGCTGAA | GGATCCT | ACAAGAA ACAAGAA | AGTACAC | AGTCGGC | TCAGGC |
| TTGCAAA | CCATTGC | TIGCCIC | GATTG | HIIII | TCAACA TCAACA | AGG# | TGAACCC TGAACCC | CAGAAGGT CAGAAGGT | ର୍ଥ – ର | TCGAGC | AAGTCAA AAGTCAA | CTGCCA | GGACGC GGACGC | GGACCG GGACCG | CCCAAAC | CAAGATA CAAGATA | GCTCTTA GCTCTTA | TAACCAA |
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| ACTGCCC | TAAC TAAC | GACTGGA GACTGGA | 13 — 13 | AATG | ATCAT ATCAT | GACAT GACAT | 6002 | ACCGIG SACCGIG | CATCC | 95555 + | GTGGA | CTGCCT | AATG | TCTATC | GAGCCT GAGCCT | ATTCCC ATTCCT | ATCGAG ATCGAG | CIGCCI |
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Sequence 3636

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                                  prior art selective markers, the gene is already expressed in all mammalian cells and the minor mutation is more natural than adding artificial gene or making major mutations so the invention is more suitable for selecting cells for transplantation into a patient. The present sequence encodes a mutated rat (Na,K)-ATPase protein where Leu at position 879 and 881 has been replaced with Tys The specification speculates that the Cys residue may form a new disulp
                                                                                                                               The invention relates to a nucleic acid encoding an ouabain-resistant (Na,K)-ATBASE termed 799/801NFA, a vector comprising the nucleic acid and a cell comprising the vector. The nucleic acid is useful as selective marker to screen for transformed cells in gene therapy Unl
                                                                                                                                                                                                                         New nucleic acid encoding an ouabain-resistant (Na,K)-ATPase for use as a selectable marker for transformed mammalian cells, particularly suitable when selecting cells for transplant into a patient -
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| ICTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACT 10 | Qy db |
| TCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAAAC | Db Qy |
| GATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTCA | ОУ |
| GCAGAGGATGTCGTCGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATC | Оу |
| AAGAACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAGAAGATGAGCATCAAC 7 | Db Qy |
| ATAACTGGCTGTTTCTCCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTT | ОУ |
| GAAGAGGAACCACCAAATGATGATCTGTACCTCGGGGTCGTGCTGCTGCTGCTGTCGTCATC 66 | Db Qy |
| ATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTACA | d dd |
| CCCCCTCCCACTACTCCCGAGTGGGTCAAATTCTGTCGGCAGCTGTTCGGTGGCTTCTCC 54 | do AA |
| GGCCTAACACCCGCAAGGGCCGCTGAGATCCTGGCTCGGGATGGCCCCAACGCCCTCACG 4 | Db dd |
| GACGACCATAAACTCAGCCTGGATGAACTCCATCGTAAATACGGAACAGATTTGAGCCG | QV Db |
| AAGAGCAAGAAGGCGAAGAAGGAAAGGGACATGGACGAACTCAAGAAGGAAG | D Qy |
| GGGAAGGGGGTTGGACGA | dd VQ |
| CTCCTCTTTCTAGTCTCCAGCCACAGGACCCGGCGCGCGGGGCCCGCAGCGCCACCA | ОУ |
| CAGCCCTAGTTCCCGCCT CAGCCCTAGTTCCCGCCT | Оу |
| GCGGCAGCAGCGGCGGCCTCGGTCCGGGGCCGGCCGGCCG | Db Qy |
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| GCCTGTG | GAAGACA | GACA | ATCACAG | TCACAG | GCTGTGGG | CTGTG | AACCTCT | CCICI | GACGAAC | GAAC | TACCTAG | ACCTAG | CICC | COTO | GCACC | AAGCACCT | AACT | TTCAACTC | TCTGCT | GTCTGCTG | ATCCTTAA | TCCTI | TCCAGAAT | CCAGAA | ACCACAGA | CCACAG | ACTCAGAA ACTCAGAA | AAGCTGT | GAAGCTGT | G- | TATGTCI | TCCT | -님 | CTGGGGGT | 13 |
| TAGTACA' | TTGCTGC | тестес | CCAAAGC | CAAAGO | GCAAATGC | CAAATG | CTTCGT | TTCGI | AGTTTCC | GTTTC | AGCTGGGGGG | - ဂို | CGGC | ACGGCAAGG | ი ი | _ ည _ | CACCAJ | CACCA | TGGCTCC | TGGCTCC | GCGTGCAG | ecerec | TGCTGGT | TGCTGGT | GAAT | GAAT | CCGGATGA | GGAG | GGAGACCTT | ACGCTC | GACGCTC | CATT | CATTGO | GICTITCIT | TCTT |
| TGGCAGTG | CCGCCTCAA | caccin | CATTGCTA | TTGCT | CGCAGCGC | CGCAG | GGGTCTTAT | -13 | CCGAAGGCTT | GAAGGCT | GGCCTTGG | -2 | AGCAGC | AGCAGC | ATGAAGG | TAGTGATGAAGGGC | ~- | CAAGTACC | TGATG | GTGATGG | GTAGCGGG | TAGCGG | CTCTGTAA | - CI | CAGAGTGGGGT | AGTGGGG | CAGTGG | GGGGT | TGGGGTC | TGCCA | ACTGCCAA | ATCATCGT | CATO | TCATTCTC | CATI |
| ACTTGAA | CATTCC | CATTCC | AAGGGGGT | | IGGGAT | IGGGAT | CTCCAT | CTCCAT | TCCAGTTT | CCAGTT | AGAGCO | AGAGCO | CCTGGA | CCCTGGAC | GCCC | GCCCCAG | 7- | CAGCTCTCC | AGATGAGG | BAGATGAGGG | AG, | AGATGO | CAGGGC | CAGGGC | CTCCTTT | CICCITI | CTCACATG | CACATO | CACATCCA | GCGCAT | GCGCATGG | AGCCAAC | - G | CTCTCTGAT | -3 |
| GGACATGA | AGTGAACC | GTGAAC | GGGCATTA | GCATT | TAAGGTCA | AAGGTC | ATTGAC | GATTGACC | GACACTO | GACACTO | G. | GCTA | AAG/ | CGAAGAGCT | AAAGGA | AAAGGA | TTC | CATTCACAAG | | GAGAAGTA | CCGAGT | CCGAGT | GIGITIC | GTGTTTC | GACAAGA | GACAAGA | GIGGITTGA | A | ACCATOTG | CGAC | GCGAGGAA | Tecces | | ATCCTTGA | CCTTG |
| ACCTCTGA | CAGGTGAA | AGGTGA | TCTCAC | TCTCAG | TCATGGT | TCATGG | CTCCTC | CTCCTCGA | ATGAAGTC | ATGA | TTTCTG | | GAAGGA | GAAGGA | TCCTGGA | TCCTGGA | AACCC | ACCC | CACCE | ACACCAAG | CGGCGCT | GGCGCT | AGGCTAA | CTAA | ACGTCAGCC | CAG | ACAATCAAAT | | GCTCCGAC | GAACTG | AGAACTGC | GGTTT | AAGGTTTG | GTACAC | GTACAC |
| GGAGCTGG | > − | CCCAGA | TAAC | GTAAC | CACAGGA | CACAGGA | GCTGCT | GCTGCT | CAATTICC | AATTI | CACCIC | CCACCTO | deciri | CGCCTTT | ccarcc | CCGATGCA | cecr | :AAACGCA: | ATAGI | SATAGTGG | CTTAAAGTG | TAAA | CCAAGAAAA | CAAC | CACCIGGI | ACCTGG | ATCCATG | AAC 16 | AAGACTG | CTGGTGA | CTGGTGA | CTGGCCA | CIGGCCA | CTGGCTCGA | - 6 - 6 |
| GATGACAT | GATGCCAA | - H - G - G | AGACCG | GAGACCGT | GACCATCC | ACCATO | Tececia | GTCCCCGA | CCGI | CCGTGG | TTCTGC | CTTCTGCC | AGAATG | CAGAATGC | GTTCTAT | GTTCTAT | ggAgc | TCGGAGCCT | AGATTO | AGATTCC | CATCGA | CATCGA | CCTGC | - C | ACCULATION OF THE PROPERTY OF | CGCTCT | AAGCTGA | ACCICI ACCICI | GAACTCT | GAACC | AGAACCTG | STCAC | CCGTCACG | AGGCTGTC | escisi |
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AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (1). (1) can have cytostatic, immunomodularrory and neuroprotective activities, and can be used in gene therapy. (1) and proteins (11) encoded by then are used in high throughput screening assays to select DNA molecules, RNA molecules, peptide nucleic acids, mimetros, poptides, proteins, aganists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (1) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (1) and (11) are used to produce an expression profile that defines a morabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis,
                                                                                                                                                                                                                                                                       New cell and tissue specific polynucleotides useful for diagnosis, progness or monitoring of treatments for disorders where the gene is associated with a cancer, immunopathology or neuropathology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 77.2%; Score 2808; DB 22; Length 8914; Local Similarity 87.1%; Pred. No. 0; es 3162; Conservative 0; Mismatches 440; Indels 30;
                         TCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAACATTGCCTTCTCTC 974
                                                                                                                                                                                                                                                                                           TCAGCAAGCCCTCGTGATTCGAAATGGAGAAGATGAGCATCAACGCAGAGGATGTCGT 794
                                                                                                                                                                                                                                                                                                                                                                            CTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTCAAGAACATGGTCCC 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATGATGATCTGTACCTCGGGGTCGTGCTGTCTGCTGTCGTCATAACTGGCTGTTT 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGAGCGATTCTTTGTTTCTTGGCTTATAGCATCCAAGCTGCTACAGAAGAGGGAACCTCA 3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGTGATAAGTATGAGCCTGCAGCTGTTTCAGAACAAGGTGATAAAAAAGGGCAAAAAAGGG 3733
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                                                                                                                                                                                                                   CGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCTGCTGATCTCAGAATCAT 854
                                                                                                                                                                                                                                                               TCAGCAAGCCCTTGTGATTCGAAATGGTGAGAAAATGAGCATAAATGCGGAGGAAGTTGT 3253
                                                                                                                                                                                                                                                                                                                                                     CTCCTACTATCAAGAAGCTAAAAGTTCAAAGATCATGGAATCCTTCAAAAAACATGGTCCC 3313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTACAGAAGAGGAACCACC 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGAGACAAGTATGAGCCCGCAGCTGTATCAGAACATGGGGACAAGAAGAGCAAGAAGAGGC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCAGCGACAGGACCCGGCCCGGGCACTGAGCACCGCCACCATGGGGAAGGGGGTTGG 3793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTGGCTCCCCTGGTCCCGCTCGCTTGGCCGGGAGCTGCTCTGTGCTTTTCTCTCTGATT 3853
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                                                                                     ATCTGCAAATGGCTGCAAGGTGGATAACTCCTCGCTCACTGGTGAATCAGAACCCCAGAC 3133
                                                                                                                 ATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTGGTGGAATCAGAACCCCAGAC 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTGAATGGATCAAGTTTTGTCGGCAGCTCTTTGGGGGGGTTCTCAATGTTACTGTGGAT 3493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCGAGTGGGTCAAATTCTGTCGGCAGCTGTTCGGTGGCTTCTCCATGTTACTGTGGAT 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Gaps
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| TC 19 | 052 TCGATAATCTGTGCTTTGTGGGCTCATCTCCATGATTGACCCTCCACGGGCGGCCGT | Д |
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| CC 203 | 976 TGGATAACCTCTGCTTCGTGGGTCTTATCTCCATGATTGACCCTCCTCGAGCTGCTGT | γQ |
| CG 1975 | 916 TGCCTGACGAACAGTTTCCCGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCC | gb Qy |
| TC 191 | 875 GGGCCTTGGAGAGCGTGTGCTAGGTTTCTGCCACCTCCT | D 9 |
| G 187 G 217 | 815 GGAGCAGCCCCTGGACGAAGAGCTGAAGGACGCCTTTCAGAATGCCTACCTA | D 49 |
| 12 18 | 55 GATGAAGGGCGCCCAGAAAGGATCCTGGACCGATGCAGTTCTATCCTCCTCCACGG | Db 9y |
| 22 | 95 CAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGGAGCCTAAGCACCTGCT | g 92 |
| A 169 A 235 | 35 CGTGATGGAGATGAGGGAGAAGTACACCAAGATAGTGGAGATTCCCTTCAACTCCAC | D Qy |
| 2 - 2 | TGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAGGTCTGCTGTGG | D Q |
| .o ⊢ .o ⊢.o | 15 TCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTGCCTATCCTTAAGCGT | Db Qy |
| 25 | 55 GAGIGGGGTCTCCTITGACAAGACGTCAGCCACCTGGTTCGCTCTGTCCAGAAITG | Db 09 |
| S=C | 95 GACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGACACCACAGAGAAT | 90 90 90 90 |
| AT 13 AT 26 | 35 CTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTGACTCAGAACCGG | Db 92 |
| AC 1334 | 75 CACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCTGGAAGCTGTGGAG | Db 09 |
| CT 1274 | 215 TATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCACGGTATGTCTGACG | 95 VQ |
| 121 283 | 55 CTTCATTCTCTCTGATCCTTGAGTACACCTGGCTCGAGGCTGTCA: | Db 09 |
| TT 1154 | 095 AGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGT | p & |
| GA 1094 GC 2953 | 035 GATGGGCF | B 64 |
| GT 1034 | 3TTGTGTACACTGGGGATCGCAC | dg Qy |

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AAGAGACAGCTCTTGCTGC1TTCCTGTCCTACTGCCCTGGGATGGGTGCAGCCCTTAGGA
                                                               GAAGGAATTCTGTCTTCCAGCAGGGAATGAAGAAGAAGATCTTAATATTTGGCCTCTTTG
                                                                                                                              CACCOTTOTTOGTOAGTATOGTOGTGGTGGAGTGGGGCTTGGTGGTCATOTGTAAGACCA
                                                                                                                                                   COGCCTTCTTTGTCASTATCSTSSTAGPSASTGGGCTGGACTTGGTCATCTGCAAGACCA
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                                                                                                                                                                                                                                                                                                           CAATTCACCTGTTGGGCCTCCGAGTGGACTGGGATGACCGCTGGATCAACGATGTGGAAG
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New cell and tissue specific polynucleotides useful for diagnosis, prognosis or monitoring of treatments for disorders where the gene associated with a cancer, immunopathology or neuropathology -

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mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of [1] in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. [1] and [1] are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH57161 to AAH57576 represent cell and tissue specific polynucleotide sequences (I). (I) can have cytostatic, immunomodulatory and neuroprotective activities, and can be used in gene therapy. (I) and proteins (II) encoded by then are used in high throughput screening
Sequence 8914 BP, 2219 A, 2249 C; 2242 G; 2204 T; 0 other;
                                                                                                                          cancer, immunopathology or neuropathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   assays to select DNA molecules, RNA molecules, peptide nucleic acids
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В В Ş DЬ á DЬ Ş ДЪ á Ş B Ş Ş Ş В 3 дδ Ş 망 В 밁 S Matches 2896; Query Match Best Local 4934 4574 4514 4394 CGGACACGTGGCAACAGCGGTACGAGCCGGGCGGCGGCAGCAACAGCGGCGGCGGCATC 4453 4874 4754 TAGCCTTGATGAACTTCATCGTAAATATGGAACAGACTTGAGCCGGGGATTAACATCTGC 4813 4814 TCGTGCAGCTGAGATCCTGGCGCGAGATGGTCCCAACGCCCTCACTCCCCCTCCCACTAC 4873 4694 CAAAAAAGACAGGGACATGGATGAACTGAAGAAAGAAGTTTCTATGGATGATCATAAACT 4753 5054 435 195 5 735 TCAGCAAGCCCTCGTGATTCGAAATGGAGAAGAAGATGAGCATCAACGCAGAGGATGTCGT 794 13 Match 70.4%; Local Similarity 87.2%; CTCGGCTCCCCGGCTCCACTCTCCCAGCCGGAGCTGCTCTCCTCCT----TTCTAGT 194 GAAGAAGGAAAGGGACATGGACGAACTCAAGAAGGAAGTGTCTATGGACGACCATAAACT 374 TGGAGCGATTCTTTGTTTCTTGGCTTATAGCATCCAAGCTGCTACAGAAGAGGAACCTCA 4993 ACGAGACAAGTATGAGCCCGCAGCTGTATCAGAACATGGGGGACAAGAAGAGCCAAGAAGGC 314 AAATGATGATCTGTACCTCGGGGTCGTGCTGTCTGCTGTCGTCATAACTGGCTGTTT 674 TCCCGAGTGGGTCAAATTCTGTCGGCAGCTGTTCGGTGGCTTCTCCCATGTTACTGTGGAT 554 CAGCCTGGATGAACTCCATCGTAAATACGGAACAGATTTGAGCCGAGGCCTAACACCCGC 434 ACGTGATAAGTATGAGCCTGCAGCTGTTTCAGAACAAGGTGATAAAAAAGGGCAAAAAAGGG 4693 CTCCAGCGACAGGACCCGGCGCGCGCACTGAGCACCGCCACCATGGGGAAGGGGGTTGG GGTCCGGGGCGCCGGCCGTCCTCTTTCC--TCCGGCGGCAGCCCTAGTTCCCGCCT 138 CTCCTACTATCAAGAAGCTAAAAGTTCAAAGATCATGGAATCCTTCAAAAAACATGGTCCC 5113 CTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTCAAGAACATGGTCCC 734 AAACGATAATCTGTACCTGGGTGTGGTGCTATCAGCCGTTGTAATCATAACTGGTTGCTT 5053 TGGAGCCATTCTTTGTTTCTTGGCTTATGGCATCCGAAGTGCTACAGAAGAGGGAACCACC 614 TCCTGAATGGATCAAGTTTTGTCGGCAGCTCTTTGGGGGGGTTCTCAATGTTACTGTGGAT Conservative 0; Mismatches 396; Indels 29; Score 2559.4; Pred. No. 0; DB 22; Length 8914; Gaps 4633

| 1813 AAGGAGCAGCCCCTGGAAGAGCCGAAGGACGCCTTTCAGAATGCCTACCTA | Db Qy |
|---|----------|
| 753 GTGATGAAGGCCCCCAGAAAGGATCCTGGACCGATGCAGTTCTA | Qy Db |
| 693 AACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGGAGGCTAAGCACCTGCTA 17 | Qy dd |
| 633 TCCGTGATGGAGATGAGGGAGAAGTACACCAAGATAGTGGAGATTCCCTT | Db 09 |
| 573 GCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAGGTCTGCTGTGGC 16 | Qy db |
| 513 GGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTGCCTATCCTTAAGCGT 157 | Qу |
| 453 CAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCTGTCCAGAATTGCT 15 | dd VQ |
| 393 ATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGACACCACAGAGAAT 14 | Оу |
| TGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTGACTCAGAACCGG 139 | QY db |
| 273 CTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGACCTGGAAGCTGTGGAG 13 | Qy Db |
| 14 GTATCATCGTAGCCAACGTGCCGGAA-GGTTTGCTGGCCACCGTCACGGTATGTCTGACG 12 | Qy db |
| 155 CTTCATTCTCTCTGATCCTTGAG-TACACCTGGCTCGAGGCTGTCATCTTCCTCATTG 12 | Дb |
| 095 AGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTTCCTGGGGGTGTG | å S |
| 35 GATGGGCAGGATCGCCACCCTTGCTTGCGCTGGAAGGCGGCCTGACCCCCATTGCTGA 10 | D 64 |
| 975 AACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACTGGGGATCGCACCGT 10 | dd VQ |
| 5 TCGGTCCCCGGATTTCACAAACGAGAAACCCCTTGGAGACAAGGAACATTGCCTTCTT | Db Qy |
| 55 ATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTCACT | Db Qy |
| 5 CGTTGGTGATCTGGTGGAGGTGAAGGGCGGAGACCGAATCCCTGCTGATGTCAA | dd VQ |
| 5114 TCAGCAAGCCCTTGTGATTCGAAATGGTGAGAAAATGAGCATAAATGCGGAGGAAGTTGT 5173 | Db |

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GGGGGCTTGGAGAGCGIGIGCT-------AGTTTCTGCCACCTCT
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2863..2940
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CC AIDS, autcimule diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders (e.g., Alzhelmer's disease, CC parkinson's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC cardiovascular disorders, angiogenic disorders, kidney disorders, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC disorders, and infections. The proteins can also be used to aid wound CC sunburn, to mainrain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. CC Antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human CC servered novelopenceding CDM of the invention can be used in the disorders mentioned above, and continuous combent assay (ELISA). The present sequence represents a human continuous combents assay (ELISA). The present sequence represents a human continuous combents assay (ELISA). The present sequence represents a human continuous 
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Best Local !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 25 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AADD17571-AADD17645 represent cDNAs corresponding to 25 human secreted protein genes, and AAED3152-AAED3126 represent the proteins they encode. AAED3127-AAED3150 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 427-428; 546pp; English.
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2911 ATAAAAAGGGCAAAAAGGGCAAAAAAAGACAGGGACATGGATGAACTGAAGAAAGTTT 2852
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                                                                                                          CCATGGGGAAGGGGTTGGACGTGATAAGTATGAGCCTGCAGCTGTTTCAGAACAAGGTG 2912
                                                                                                                                                                                                                                                                                                                                CCATGGGGAAGGGGGTTGGACGAGACAAGTATGAGCCCGCAGCTGTATCAGAACATGGGG 295
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| FIFATUUACATUATATOAGGIGIGGETG 20 | 1 GCCAGACCCCCATTGCTGCAGAAATTGAACATTTT | DЬ |
| TTCATCCACCTCATCACGGGTGTGGGCCG 113 | 076 GCCTGACCCCCATTGCTGAAGAAATCGAGCAC | 8 |
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| CCACCCTTGCTTCTGGGCTGGAAGGCG 1 | 016 ACACTGGGGATCGCACCGTGATGGGCAGGATCGCC | Qy |
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| TGCAAGGTGGATAACTCCTCGCTCAC | 71 CTGCTGACCTCAGAATCATATCTGCAAATGGCT | |
| TGCAAGGTGGATAACTCCTCACTG 89 | 36 CTGCTGATCTCAGAATCATATCTGCAAATGGCT | Qy |
| TGGAAGTAAAAGGAGGAGJ | 31 TAAATGCGGAGGAAGTTGTGGTTGGGGATCTG | |
| TGGAGGTGAAGGGCGGAGACCGAATC | 76 TCAACGCAGAGGATGTCGTCGTTGGTGATCTG | γŞ |
| GTGATTCGAAATGGTGAGAAAATGAGC | 91 CCTTCAAAAACATGGTCCCTCAGCAAGCCCTTG | |
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| GAAGCTAAAAGTTCAAAGATCATGGAA | 51 TAATCATAACTGGTTGCTTCTCCTACTATCAAGAA | |
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| AAATTCTGTCGGCAGCTGT | 476 TCACGCCCCTCCCACTACTCCCGAGTGGGTCAA | |
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IET 16-SEF-2002 (first entry)

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IEE Human prostate expression marker
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EM Homo sapiens.
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OS Homo sapiens.
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OS Homo sapiens.
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PN W0200160860-A2.
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PD 23-AUG-2001.
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PD 23-AUG-2001.
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PD 29-EBP 2001; 2001W0-US05171
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PR 17-EBB-2000; 2000US-183319P.
PF 15-MAY 2000; 2000US 201314P.
PR 18-JUL-2000; 2000US-219007P.
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Best Local Similarity
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(e) selecting
(f) assessing
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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(d) assessing the efficacy of a therapy for inhibiting prostate cancer
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   1293 GA-GGAAGAACTGCCTGGTGAAGAACCTGGAAGCTGTGGAGACCTTGGGGTCCACATCCA 1351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound;
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                                                                GGAAGGTTTGCTGGCCACGTGTCACGGTCTGTCTGACACTTACATTGCAAACTGCATGGC 5709
                                                                                                                                                                                 AGTACACCTGGAATTGAGGCTGTCATCTTCCTCATCGGTATCATCGTAGCCCAATGTGCC 5769
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86.4%; Pred. No. 0;
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16-MAY-1000; 2000US-109962P.
25-MAY-2000; 2000US-207454P.
19-JUL-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
19-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification of its complement, (1) is useful for (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3427
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                                                                                                                                                                                               cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patien;
(f) assessing the prostate cell carcinogenic potential of a compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel implated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for derecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; piostate dander; dytostatic; dardinggen; pharmadodyanamic marker; pharmacogenomic marker; gene; ss.
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                                                                patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 6171-6173; 11750pp; English.
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      Seguence
                                                                                                                              selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCGGAAAGACTGAAAGAATACATTTATATCTGGATTTTTACAAATAAAGATGGCTATT
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          1488 A, 1621 C, 1619 S,
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             ) other,
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| 772 AAAG | 8 |
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| 1712 TTCACAAGAACCCAAACGCATCGSAGCCTAAGGACCTGCTAGTGATGAAGGGCGCCCAG 1771 | 40 |
| 1652 AGAAGTACACCAAGATAGTGGAGATTCCCTTCAACTCCACCAACAAGTACCAGCTCTCCA 1711 | 90 VQ |
| ი—ი - | P 6 |
| 1532 TGTTTCAGGCTAACCAAGAAAACCTGCCTATCCTTAAGCGTGCAGTAGCGGGAGATGCTT 1591 | g 8 |
| 1472 ACAAGACGTCAGCCAGCTGGTTCGCTCTGTCCAGAATTGCTGGTCTCTGTAACAGGGCAG 1531 | 8 8 |
| 1412 GGTTTGACAATCAAATCCATGAAGCTGACACCACAGAGAATCAGAGTGGGGGTCTCCTTTG 1471 | 90 VO |
| 1352 CCATCTGCTCCGACAAGACTGGAACTCTGACTCAGAACCGGATGACAGTGGCTCACATGT 1411 | 9d 6 |
| 1293 GA-GGAAGAACTGCCTGGTGAAGAACCTGGAAGCTGTGGAGACCTTGGGGTCCACATCCA 1351 | 90 80 |
| 1236 GJAAGGTITGCTGGCCAC-CGTCACGGTATGTCTGACGCT -CACTGCCAAGCGCATGGC 1292 | 8 6 |
| 1178 AGTACACCTGG-CTCGAGGCTGTCATCTTCCTCATTGGTATCATCGTAG-CCAACGTGCC 1235 | B 8 |
| 1118 TCATCACGGGTGTGGCCGTGTTCCTGGGGGGTGTCTTTCTT | Db |
| 1058 CTTCTGGGCTGGAAGGCGGCCTGACCCCCATTGCTGAAGAAICGAGCACTTCATCCACC 1117 | 8 |
| 998 CACGTGGCATCGTTGTGTACACTGGGGATCGCACCGTGATGGGCAGGATCGCCACCCTTG 1057 | 8 |
| 938 AGAACCCCTTGGAGACAAGGAACATTGCCTTCTTCTCAACCAAC | B & |
| 878 ATAACTCCTCACTCACTGGTGAATCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACG 937 | P 64 |
| 820 GGCGGAGACCGAATCCCTGCTGATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGG 877 | d V |
| 760 GGAGAGAAGATGAGCATCAACGCAGAGGATGTCGTCGTTGGTGATCTGGTGAAGGTGAAG 819 | do Vo |
| 86.4%; Pred. No. 0; ive 0; Mismatches | 3 00 |

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| 852 TTCTGGCTGAGAACGGTTTCCTGCCCTTTCACCT | 792 TGGCCTATGGACAGATCGGTATGATCCAGG | 732 TGANGAGGCAGCCCAGNAATCCCNAAACGI | 1 GGGCACTGACATGGTTCCCGCCATCTCCCTGG | blz TATTTATTATTGCAAACATTCCACTACCACTGG | 552 TGAAGAAATCCATTGCTTACACCCTAACA | 192 ATGACAACTTTGCCTCCATCGTGACTGGAGTAC | 32 TIGCCATGGGGATTGTTGGCT | 72 TGGCTGTCACAGGGGATGGTGAATGACTC | 12 GGACCTCTCCTCAACAGAAGCTCATCATTC | 52 ACATGACCTCTGAGGAGCTGGATGACATTTTGG | 92 TGAACCAGGTGAACCCCAGAGATGO | 32 GCATTATCTCAGAAGGTAACGAGACCGTGGAAGJ | 72 AGGTCATCATGGTCACAGGAGACCATCCAATCA | 12 TEGACCOTCCTCGACCTGCTGTCCCGATGCTC | 52 ACACTGATGAAGTCAATTTCCCCGTGGATAACC | 08 TCCTAGGTTTCTGCCACCTCTTCTGCCAGAIGA | 68 AGGAGCTGAAAGACGCCTTTCAGAACGCCT | 32 AAGAGCTGAAGGACGCCTTTCAGAA | 28 AAAGGATCCTAGACCGTTGCAGCTCTATCCTCCT |
| TGTTGGGCATCCGAGAGACCTGGGATG 2911 TGTTGGGCCTCCGAGTGGACTGGGATG 4089 | CTTCTTCACTTATTTTGTGA 285 | SAACGAGCGTCTGATCAGCA 2/9 SAATGAGCGGCTGATCAGCA 420 | CTTATGAGCAGGCTGAGAGTGACATCA 426 | ACCEPTANCE OF THE PROPERTY OF | ATTCCGAAATCACCCCTTCTTGA 261 | ngaaggtcgtctgatatttgataact 255 gaaggtcgtctgatcttgataact 444 | GCAAGCTGCTGACATGATTCTTCTGG 24 | GCTTTGAAAAAGGCAGATATTGGGG 243 GCTTTGAAGAAAGCAGACATTGGGG 456 | AGGGCTGCCAGCGGCAGGGTGCCATCG 237 | TACCACACGGAGATTGTCTTTCCTA 23 | GTAGTACATGGCAGTGACTTGAAGG 225 GTAGTACACGGCAGTGATCTAAAGG 474 | CATTGCTGCCGCCTCAACATTCCAG 21 | G 48 | GCAAATGTCGAAGTGCTGGAATTA 49 | CTGCTTCGTGGGTCTTATCTCCATGA 2 | CAGTTTCCTGAAGGGTTCCAGTTTG 504 | AGCTGGGGGGGCCTCGGAGAA AGTTTCCCGAAGGCTTCCAC | \GCTGGGGGGCCTTGGAGAGCGTG 189 | CCACGGCAAGGAGCAGCCCCTGGATG 5169 |

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           Homo sapiens
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                                  leukaemia; ss.
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                                          drug screening,
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Best Local 9
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09-JUL-2000, 2006US-058042.
19-JUL-2000, 2006US-0653450.
34-SEP 2000, 2006US-0653356.
19-OCT-2000, 2006US-0693356.
23-MUV-2160, 2606US-0727744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642 AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3526 BF; 726 A; 1134 C; 961 G; 705 T; 0 other;
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25-APS-2000;
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P-PSDR; AAM39149
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   601 GAAGAGGAACCACCAATGATGATTATATCTTCBSGGTCGTGCTGTCTGTTGTTGTCATC
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Zhou P,
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77.2%;
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Pred. No. 0;
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Ener
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                                                                                                                                                                                                                                    Human prhymucleottide SEC 15 NO 2404.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation.
Note. Records for SEQ ID NO 2110 (AAK1218), 2111 'AAK12192) and 2666 (AAK80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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DB; AAM79742.
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                                                     ATCACTGGCTGCTTCTTCCTACTACCAGGAGGCTAGGAGAGCTCCAAGATGATGGGTCCTTTC
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Yang Y, Wejbrman
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| 1918 CCTGACGAACAGTTTCCCGAAGGCTTCCAGTTTGACACTGATGAAGTCAATTTCCCCGTG 1977 | Оу |
| 1858 GCCTACCTAGAGCTGGGGGGCCTTGAAGAGCGTGTGCTAGGTTTCTGCCACCTCCTTCTG 1917 | dd VQ |
| 1798 ATCCTCCACGGCAAGGAGCAGCCCCTGGACGAAGACTGAAGGACGCCTTTCAGAAT 1857 | do VQ |
| 1738 CCTAAGCACCTGCTAGTGATGAAGGGCGCCCAGAAAGGATCCTGGACCGATGCAGTTCT 1797 | Оу |
| 1678 CCCTTCAACTCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGGAG 1737 | dq VQ |
| 1618 GAGGTCTGCTGTGGCTCCGTGATGGAGGAGATGAGGGAGAAGTACACCAAGATAGTGGAGATT 1677 | g 99 |
| 1558 CCTATCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATC 1617 | Db Db |
| 1500 GTCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTG 1557 | Qy Db |
| 1440 CACCACAGAGAATCAGAGTGGGGTCTCCTTTGACAAGACGTCAGCCACCTGGTTCGCTCT 1499 | ОУ |
| 1380 GACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCAAATCCATGAAGCTGA 1439 | Qy dd |
| 1320 GGAAGCTGTGGAGACCTTGGGGGTCCACATCCACCATCTGCTCCGACAAAGACTGGAACTCT 1379 | Qy |
| 1260 GGTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCT 1319 | ОУ |
| 1200 CATCTTCCTCATTGSTATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCAC 1259 | Db Qy |
| 1140 CCTGGGGGTGTCTTCTTCATTCTCTCTCTGATCCTTGAGTACACCTGGCTCGAGGCTGT 1199 | Оу |
| 1080 GACCCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTT 1139 | Оу |
| 1020 TGGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTG | Db Oy |
| 960 CATTGCCTTCTCCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTACAC 1019 | Db dd |
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| CTIC | TCAGTATCG | AGCAGTGGACC' AGCAGTGGACA' | TTGGGCATCCC GTGGGCATCCC | SAGGCTTCTTCAC STGGCTTCTTCTC | AAACTTGTGAACGAGCGTCTGAT AAATTGGTCAATGAGAGACTCAT | ATGAACAGGCTO | CATCACC | ΩΩ | ര — ഒ | CAAGCAAGCTGCTGACATGATTCTT | AGCTTTGAAAAAGGCAG CGCTCTGAAGAAGGCCG | JAGGGCTGCCAGCG JAGGGCTGTCAGAG | CGGTACCACGGAGATTGTCTT | TAGTACATGG | CATCGCCGCCGC | CCAAAGCCATTGCTAAGGGGGTGGG | TGGGCAAATGCCGCAGCG TGGGCAAGTGTCGCAGCG | CTTTGTGGG |
| CAGCAGGGAATGAAGAACAAGATCTTAATATTTGGC | CGTGGTAGTGCA CGTTGTCGTCCA | TACGAGO | CGAGAGACCTG | 뭐ㅡㅂ | GCGTCTGAT | JAAAG JAAAG | ATCCTCTGCATTGACTTGGGC | CGGAAATCACCCCCTTCTT CGGAGATCACGCCCTTCCT | GATATTIGA GATCTTCGA | CATGATTCT | № — № | CAGCGGCAGGGTGC CAGAGACAGGGTGC | GATTGTCTT | CATGGCAGTGACTTGAAGGACATGACCTCTGAGG | GCCCGCCTCAACATTO | TGCTAAGGG TGCCAAGGG | CAGG | CCTCATGTC |
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| 981 AACCTCTGCTTCGTGGGTCTTATCTCCATGATTGACCCTCCTCGAGCTGCTGTCCCCGAT 204 | |
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                                                                                                     CCTTTTTGTTTTTGTAAAAAAGGAAAACCTGGAAAGACTGAAAGATTACGTTTTATATCT 3600
                                                                                                                                              GGGGAGGGCTGCCCGAAAAAACACCGTGGACGGGGACGACAGCGGGGAAGGTTTATATGTG
                                                                                                                                                                               GGGGAGGGCTGCCCGAAAAAACACCGTGGACGGGGACGACAGCGGGGAAGGTTTATATGTG
                                                                                                                                                                                                                     CCAAAGCATGTGGGGATCCAGACGTCCTGGAATGAAGCATGTAGCTGTAATGGGGGGGCGG
                                                                                                                                                                                                                                                                                           TACCCCCCTTTGTGTACTTCAAGTCTTGGAGCTCGGAACTCTACCCTGGTAGGAAAGCA 3420
                                                                                                                                                                                                                                                                                                                                                                 TACTACTAGCCCACTGCCCTGCACGCCGTGGAACATTGTGCCACACACTGCACCTACCCC
                                                                                                                                                                                                                                                                                                                                                                                                  TACTACTAGECCACTGECCTGEACGECGTGGAACATTGTGECACACACACTGCACCTACECE 3360
GGATTTTTACAAATAAAGATGGCTATTATAACGGAA 3636
                                                                      CCTTTTTGTTTTTGTAAAAAAGGAAAACCTGGAAAGACTGAAAGATTACGTTTTATATCT
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SEQ ID NO 5
LENGTH: 3636
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TITLE OF INVENTION: SELECTION MARKER
FILE REFERENCE: BELUSA 09/090,535
CURRENT APPLICATION NUMBER: US/09/090,535A
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: US 60/048,601
EARLIER EILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTTACTGTGGATTGGAGCCATTCTTTGTTTGTTGGCTTATGGCATCCGAAGTGCTACA
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AAGAACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAGAAGATGAGCATCAAC
                                                                                            ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC
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| 1860 | 1801 CTCCTCCACGGCAAGGAGCACCCCTGGACGAAGAGCTGAAGGACGCCTTTCAGAATGCC | Å, |
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| 1800 | 1741 AAGCACCTGCTAGTGATGAAGGGCGCCCAGAAAGGATCCTGGACCGATGCAGTTCTATC | д 9 |
| 1740 1740 | 1681 TTCAACTCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCAAACGCATCGGAGCCT : | 8 |
| 1680 1680 | 21 GTCTGCTGTGGCTCCGTGATGGAGATGAGGGGAGAAGTACACCAAGATAGTGGAGATTCCC | dd Gy |
| 1620 1620 | 61 ATCCTTAAGCGTGCAGTAGCGGGAGATGCTTCCGAGTCGGCGCTCTTAAAGTGCATCGAG | g 82 |
| 1560 1560 | 1501 TCCAGAATTGCTGGTCTCTGTAACAGGGCAGTGTTTCAGGCTAACCAAGAAAACCTGCCT : | d Qy |
| 1500 1500 | 1441 ACCACASAGAATCAGASTSSGGTCTCCTTTGACAAGACGTCAGCCAGCTGGTTCGCTCTG : | gg Vg |
| 1440 1440 | 1381 ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAATCCATGAAGCTGAC: | 99 29 |
| 1380 1380 | :321 GAAGUTGTGGAGACCITGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG: | 8 8 |
| 1320 1320 | 261 GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAAGAACTGCCTGGTGAAGAACCTG | B 8 |
| 1260 1260 | :201 ATCTTCCTCATTGGTATCATCGTAGCCAACGTGCCGGAAGGTTTGCTGGCCACCGTCACG 1 | p & |
| 1200 | 1141 CTGGGGTGTCTTTCTTCATTCTCTCTCTGATCCTTGAGTACACCTGGCTCGAGGCTGTC 1 | P Q |
| 1140 1140 | 1081 ACCCCCATTGCTGAAGAAATCGAGGACTCATCACCTCATCACGGGTGTGGCCGTGTTC 1 | P Ç |
| 1080 1080 | 1021 GGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTCTGGGCTGGAAGGCGGCCTG : | do do |
| 1020 | 961 ATTGCCTTCTCTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTACACT 1 | P 99 |
| 960 | 901 TCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAAC (| р 8 |
| 900 | 841 GATCTCAGAATCATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTGACTG | 95 85 |
| 840 840 | 781 GCAGAGAGATGTCGTCGTTGGTGATCTGGTGGAAGTGAAGGGCGAAGACCGAATCCCTGCT 8 | 8 |
| 780 | | Db |

| 1861 TRICTICACGGCAMAGAGCTTGAMAGAGCTGAMAGAGCTGAMAGACCACTTTTCAGATTGCC 188 1861 TRICTIMAGAGTTGAGGCCCCTTGGAGAGAGCTGAMAGACCACTTTTCAGATTGCC 188 1861 TRICTIMAGAGTTGAGGCCCCTTGGAGAGCTTGAGAGCTTGAGAGTTCAGACTTGCCCTTGCCT 199 1861 TRICTIMAGACTGAGGGCCTTGGAGAGCTTCAGAGTTCAGACTTCAGACTTCAGACTTCAGAGTTGAGCTTGAGAGTTGAGAGTTGAGAGTTGAGCTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGAGCCCTTCCTT | | | | | | | | | | | | | | - | | | | | |
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| TCCTCCACGGGGAGGGGCTTGGAGGAGGGTTGGTAGGAGGGCTTTCAGAATGCC TRACCTAGACTGGGGGGGCTTGGAAGGCTTGAGAATGCC TRACCTAGACTGGGGGGGCTTGGAGGAGGCTTGAGACTGCTTCCCCCTTCTGCCT TACCTAGACGCTGGGGGGGCTTGGAGGAGGCTTGAGACTCCTTCTGCCCT TACCTAGACGCTTCCCAAAGGCTTCCAGAGTTGACCCTCCTTCTGCCCCT TACCCACCAACGCTTCCCAAAGGCTTCCAGATTGACCCTCCTCCTCCAGAGTCCAACCCTCCTCCCCCAACCCCTTCCTCCCCAAAGCCCAAACCCCTTGCTAACCCTCCTAAAGGTCAAAACCCATTGCTCAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAACCATTGCTAAAAACCATTGCTAAAAAAAA | DB QY | Db Oy | Db Oy | Db Oy | B 8 | Db Qy | Db Qq | 90 VQ | A 4 | Db Qy | Db Qy | P 64 | dd VQ | Db Qy | B 84 | Db Qy | D Qy | B 09 | В |
| COGCANGGAGCACCCCTGGACGAAGAGCTGAAGAGCTGAAGAACACCTCCTTCCAGAATGCC 19 20 TICLICIA IIII IIII IIII IIII IIII IIII II | 9 8 | 0 00 | 2761 2761 | 2701 2701 | 2641 2641 | un un | (I) | 4 6 | 0 0 | 41 | 2281 | () () | 2161 2161 | 0 0 | | | 12 10 | 1861 1861 | 8 |
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GENERAL INFORMATION:
APPLICANT: BELUSA, ROGET
ITITE OF INVENTION: SELECTION MARKER
FILE REFERENCE: BELUSA 09/090,535
CURRENT APPLICATION NUMBER: US/09/090,535A
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: US 60/048,601
EARLIER FILING DATE: 1997-06-04
NUMBER OF SEO ID NOS: 18
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                                                           SOFTWARE: PatentIn Ver. 2
SEQ ID NO 6
LENGTH: 3636
TYPE: DNA
ORGANISM: Rattus rattus
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Matches 3630;
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| מסופס מסת מחדיבית מנית ליחיים מחדיב בינים בינים מחדיב בינים בינים מחדיבים מודיבים מודים מודים מודיבים מודיבים | 2101 ATCACAGG | ्र |
| SECTADA NACIOS ASSISTEGRATTARGRICATE ALGERICAGAGA GACCATCON 2100 | 2041 GCTGTGGG 2041 GCTGTGGGGG | 40 |
| TGOTTOCTANATOTACTOCATSACTCATCAGGTTCATCGAGTGGTCTCGAGTOCAGGTCCTCGAGTCAGGTCTCGAGGTTCAGGTCTCGAGGTCGCCGAT 2040 | 1981 AACCTCTG 1981 AACCTCTGG | DP CSA |
| A-WITTO-OGSANSSCIPSCASTIFSALACTSATSAAGTCAATTCCCCGTGGAT 1980 | 1921 GARGAARA 1921 GARGAARA | Db OY |
| ACAGERGAGGGACTEGAAGAGGTGTGTGTGAGAGTTEGGCAGGTCCTTCTGCTT 1920 | 1861 TACCTAGAC | B 4 |
| | 1801 CTCCTCCAC | d d d |
| PETBELAS PSA PSAASSESEECE CASAAASSA PETBESA CEGATECASTECTATE 1800 | 1741 AAGCACCTO 1741 AAGCACCTO | Фр |
| TTECHCCAACHAGTACCASCTCTECHTTCACAAGAACCCAAACSCATACSSAGCCT 1740 | 1681 TTCAACTCG | 44 |
| TPOTOGOTOGOTSATOGAGATGAGGGAGAAGTACACCAAGATAGTGGAGATTCCC 1680 | 1621 GTCTGCTGT | dp 2y |
| PANGUGTUCAGIAGCOGGAGAIGCTICCGAGICOGUGCTCTIAAAGIGGATCGAG 1620 | 1561 ATCCTTAA: 1561 ATCCTTAAC | å Ç |
| WITTSCTSSICICTSTANCASSSCASISTITCASSCIAACCAASAAAACCISCCT 1560 | 1501 TOCAGAATT | Db dq |
| NSASAATCASASTSSSSTCTCCTTTSACAASACSTCASCCACCTSSTTCSCTCTS 1500 | 1441 ACCACAGAG 1441 ACCACAGAG | Dr S |
| BARCOSSAISACASTSSCTCACATSTSSTTIGACAAICAAATCCAIGAASCIGAC 1440 | 1381 ACTCAGAAC 1381 ACTCAGAAC | 4 <u>0</u> |
| ROTOGAGACCITEGGGICCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG 1380 | 1321 GAAGCTGTG 321 GAAGCTGTG | d Qy |
| CTSACSCTCACTSCCAASCSCATESCSASSAASSACTSSCTSSTBAAGAACCTG 1320 | 1261 GTATGTCT0 1261 GTATGTCTC | dd Yo |
| TTCATTGSTATCATGSTAGCCAAGGTGSGGAAGGTTGCTGGGCCACGTCAGG 1260 | 1201 ATCTTOCTC | gg Qy |
| RETETOTITETECATICTETETETESATECTTGAGEA-ACTGEGETGGAGGCTGTO 1200 | 1141 (TBRARETO 1141 (TBBARETO | g & |
| 081 ACCCCCATERCTAAAGAAGCAACACTAATCACCCCCATCACCGGTGTGGCCGTGTTC 1140 | 1081 ACOCCTATI | 4C V |

| 81 ACTCAGAACCGGATGACAGTGGCTCACATGTGGTTTGACAATCAAT | - Q | Db 241 GGAAGGGGGTTGGACGAGACAAGTATGAGCCCGCAGCTGTATCAGAACATGGGGACAAG 300 Qy 301 AAGAGCAAGAAGGCGAAGAAGGGAAAGGGACATGGACGAACTCAAGAAGGAAG |
|--|----------|--|
| 1321 GAAGCTGTGGAGACCTTGGGGTCCACATCCACCATCTGCTCCGACAAGACTGGAACTCTG 1380 | Qy Db | Qy 241 GGGAAGGGGTTGGACGAGACAAGTATGAGCCCGCAGCTGTATCAGAACATGGGGACAAG 300 |
| GTATGTCTGACGCTCACTGCCAAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACCTG 1 | Db ci | Qy 181 CTCCTCTTTCTAGTCTCCAGCCACAGGACCCGGCGGGGGGCCGCAGCGCGCAGCGCATG 240 |
| ATCTTCTCATCGTATCATCGAAGGCCAAGGCGGGAAGGAA | Db & | Qy 121 CAGCCTAGTTCCCGCCTCTCGGCTCCCCGGGTCCACTCTCCCAGCCGGGAGCTGCTCT 180 |
| 1141 CTGGGGTGTCTTCATTCTCTCTCTCTGATCCTTGATGTACACCTGGCTCGAGGCTGTC 1200 | S | Qy 61 GCGGCAGCAGCGGCGGCCTCGGTCCGGGGGCCGGCCGTCCTCTTTCCTCC |
| 1081 ACCCCCATTGCTGAAGAAATCGAGCACTTCATCCACCTCATCACGGGTGTGGCCGTGTTC 1140 | Оу | SCTCGGCGGAGGAGGCGGACACGTGGCAGCGGCGGCGGCAGCAGCAGCAGCAGCAGCGGCGGCAGCA |
| 1021 GGGATCGCACCGTGATGGGCAGGATCGCCACCCTTGCTTG | 0; da | 99.6%; Score 3621.6; DB 4; Length 3636; imilarity 99.8%; Pred. No. 0; ; Conservative 0; Mismatches 9; Indels 0; Gaps |
| 961 ATTGCCTTCTCAACCAACTGTGTTGAAGGAACT3CACGT3GACTGTGTGTGTACACT 1020 | Су | LENGTH: TYPE: DN ORGANISM S-09-090-53 |
| 901 TCAGAACCCCAGACTCGGTCCCCGGATTTCACAAACGAGAACCCCTTGGAGACAAGGAAC 960 | Qy | EARLIER FILING DATE: 1997-06-04 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PAtentin Ver. 2.0 SEO ID NO 7 |
| 841 GATCTCAGAAICATATCTGCAAATGGCTGCAAGGTGGATAACTCCTCACTCA | QУ | FILE REFERENCE: BELUSA 09/090,535 ; CURRENT APPLICATION NUMBER: US/09/090,535A ; CURRENT FILING DATE: 1998-06-04 ; EARLIER APPLICATION NUMBER: US 60/048.601 |
| 781 GCAGAGGATGTCGTTGGTGATCTGGTGSAGGTGAAGGGCGGAGACCGAATCCCTGCT 840 | Qy | |
| 721 AAGAACATGGTCCCTCAGCAAGCCCTCGTGATTCGAAATGGAGAAGAGGAGAGAGCATCAAC 780 | Qy Db | RESULT 4 US-09-090-535-7 : Sequence 7. Application US/09090535A |
| 661 ATAACTGGCTGTTTCTCCTATTATCAAGAAGCAAAAAGCTCCAAGATCATGGAATCCTTC 720 | Qy | QY 3601 GGATTTTTACAAATAAAGATGGCTATTATAACGGAA 3636 |
| 601 GAAGAGGAACCACCAAATGATGATCTGTACCTCGGGGTCGTGCTGTCTGCTGTCATC 660 | Qy | OY 3541 CCTTTTTGTTTTTGTAAAAAGGAAAACCTGGAAAGACTGAAAGATTACGTTTTATATCT 3600 |
| 541 ATGTTACTGTGGATTGGAGCCATTCTTTGTTTCTTGGCTATGGCATCCGAAGTGCTACA 600 | Qy | Qy 3481 GGGAGGGCTGCCCGAAAAACACCGTGGACGGGACGACAGCGGGGAAGGTTTATATGTG 3540 |
| 481 CCCCCTCCCACTACTCCCGAGTGGGTCAAATTCTGTCGGCAGCTGTTCGGTGGCTTCTCC 540 | Çy Db | OY 3421 CCAAAGCATGTGGGGATTCCAGACGTCCTGGAATGAAGCATGTAGCTGTAATGGGGGGGCGG 3480 |
| 421 GGCTAACACCCGCAAGGGCCGCTGAGATCCTGGCTCGGGATGGCCCCAACGCCCTCACG 480 | Qy | OY 3361 TACCCCCCCTTTGTGTACTTCAAGTCTTGGAGCTCGGAACTCTACCCTGGTAGGAAAGCA 3420 |
| 361 GACGACCATAAACTCAGCCTGGATGAACTCCATCGTAAATACGGAACAGATTTGAGCCGA 420 | dd VQ | QY 3301 TACTACTAGCCCACTGCCCTGCACGCCGTGGAACATTGTGCCACACACTGCACCTACCCC 3360 |
| 301 AAGAGCAAGAAGGCGAAGAAGGAAAGGGACATGGACGAACTCAAGAAGGAAG | ם סב | Db 3241 GACGAGGTGCGGAAGCTCATCATCAGGCGACGCCCTGGCGGCTGGGTGGAGAAGGAAACC 3300 |

| | 6) () | da Ab |
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| GAGATTGTTGGCTCGGATGTG 2460 | N N | D KY |
| | N N | ψy |
| TCCTCAACAGAAGCTCATCATT 2340 | KI D | d d d |
| CTCTGAGGAGCTGGATGACATT 2280 2280 TTCTGAGGAGCTGGATGACATT 2280 | ta ta | αα (3. |
| GGTGAACCCCAGAGATCCCAAG 2220 | ro ti | S. S. |
| CTCAGAAGGTAACGAGACCGTG 2160 | (A).A | g oy |
| CATGGTCACAGGAGACCATCCA 2100 | N N | 4 5 |
| ICCTCSAGCTGCTGTCCCCGAT 2040 | ע ע | dc YO |
| FGAAGTCAATTTCCCCGTGGAT 1980 | بر بر | ОУ |
| | н н | 8 8 |
| 3AA34A737CTTTCAGAATGCC 1860 AA33ACGCCTTTCAGAATGCC 1860 | <u>, , , , , , , , , , , , , , , , , , , </u> | ψy |
| CCT93ACCGATGCAGTTCTATC 1800 | ⊢ ⊢ | ОУ |
| 3AACCCAAACGCATCGGAGCCT 1740 3AACCCAAACGCATCGGAGCCT 1740 | <u> </u> | 04 04 |
| CACCAAGATAGTGGAGATTCCC 1680 ACCAAGATAGTGGAGATTCCT 1680 | L | Oy Dh |
| 39090T0TTAAA3T30AT0GAG 1620 39090T0TTAAAGTGOATGGAG 1620 | | DB GA |
| 990TAA00AAAAA00TGCCT 1560 | jun | 65 65 |
| | | Cy |

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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-266XX
CURRENT APPLICATION UNMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-08-08
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/98,639
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER: OF SEQ ID NOS: 544
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US-09-385-982-501
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APPLICANT: ENDEGE, WILSON O., ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.5%;
Best Local Similarity 85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (1) (605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2288 ACCACACGGAGATTGTCTTTGCTAGGACCTCTCCTCAACAGAAGCTCATCATTGTGGAGG 2347
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                                                                                                                                                                                               361
474 CTTGTGAATGANCNGGTGATCA 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTCCATCGTGACTGGAGTAGAAG 2527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCGTGACCATCCTCTGCATTGACTTGGGCACTGACATGGTTCCCGGCCATCTCTCTGGGC 2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GÉTGCÉAAAGACÁGGGTGCTÁTCGTGGCTGTGACTGGTGACGGTGTGAATGACTCTCCAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCACACTGAGATAGTGTTTGCCAGGACCTCCCCTCAGCAGAAGCTCATCATTGTGGAAG 60
                                                                                                                                                                                                                                                                                                                              TT-CCGGAAATCACCCCCTTCTTGATATTTATTATTGCAAACATTCCACTGCCCCTGGGC 2646
                                                                                                                                                                                                                                                                                                                                                                                       AAGGTCGTCTGATCTTTGATAACTTGAAAAAATCCATTGCTTATACCTTAACCAGTAACA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGTCGTCTGATATTTGATAACTTGAAGAAATCCATTGCTTACACCCTAACAAGTAACA 2587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĆŤŦŦĠĄĄĠĄĄĄĠĊĄĄĄĊĄŦŦĠĠĠĠŦŦĠĊŦĄŦĠĠĠĠĄŦŦĠĊŦĠĠĊŦĊĄĠĄŦĠŦĠŦĠŦĊĄĄĄĠĊ 180
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                                                                                                                                    TATGAACAGGCTGAAAGTGACATCATGAAGAGGCAGCCCAGAAATCCCCAAAACGGACAAA 2766
                                                                                                                                                                                                                                                                                            TTCCCCGAGATCACCCCGTTCCTGATATTTATTATTGCAAACATTCCACTACCACTGGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCTGCTGACATGATTCTTCTGGATGACAACTTTGCCTCAATTGTGACTGGAGTAGAGG 240
                                              CTTGTGAACGAGCGTCTGATCA 2788
                                                                                               TATGAGCAGGCTGGA--GGGCATCATGAANAAACAGCCCAAAATCC----AAACAGACAA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 344.4; DB 4; Length 605; Pred. No. 6.7e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Indels
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US-08-961-527-55/c
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3.7%; Score 133; DB 4; Length 21040;
Best Local Similarity 53.9%; Pred. No. 1.5e-24;
Matches 321; Conservative 0; Mismatches 265; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2162 AAGACATTGCTGCCGGCCTCAACATTCCAGTGAACCAGGTGAACCCCAGGAGATGCCAAGG 2221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: mEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1875 AAGACACAGCGGAAGCCATTGCCAAACGTTTGGGAATCATTGACGCAAACGATACAGAAG 1816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1755 TTGGTCAATACTC----TGTTTATGCCCGTGTGTCTCCAGAACACAAGGTTCGTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1815 GTCACGTTTTAACTGGTGCTGAACTCAATGAACTGTCAGATGAAGAATTTGAAAAAGTCG 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2222 CCTGTGTAGTACATGGCAGTGACTTGAAGGACATGACCTCTGAGGAGCTGGATGACATTT 2281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
2522 TAGAAGAAGGTCGTCTGATATTTSATAACTTGAAGAAATCCATTGCTTACACCCTAACAA 2581
                                                                                                                                             1581 CTAAGGGGGCTTCTGATATGATTCTTGCAGATGATAACTTTGCGACTATTATCGTCGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCAGCTTTGAAAAAAGGCAGATATTGGGGTTGCCATGGGGATTGTTGGCTCGGATGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGGGCTGCCAGCGGCAGGGTGCCATCGTGAGCTGTCACAGGGGATGGTGTCAATGACT 2401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCGGTACCACACGGAGATTGTCTTTGCTAGGACCTCTCCTCAACAGAAGCTCATCATTG 2341
                                                                                                                                                                                                                                                                                                                                 CGCCAGCTCTGAAAACAGCCGATATCGGTATCGGTATGGGAATCACTGGTACAGAGGTTT
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Maryland
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                                                                                                                                                                         Best Local Similarity
Matches 256; Conserv
                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                  C9-958.207A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, Dayid
                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ IT NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAME. Gimmi, Edward R
REGISTRATION NUMBER: 38,991
REFERENCE/POCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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                                                                                    1090 AAGAMAMAGDARAAGCMATTGCCAAAMGGTTTGGGAAATCAITGAGGCAAACGAIACAGAAG 1031
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MEDIUM TYPE. Diskett
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1030 GTCACGTTTTAACTGGTGCTGAACTCAATGAACTGTCAGAFGAAGAAGTTTGAAAAAAGTUG 971
                                   2011 OF THE TRAITMENTAL WITHAM THAN A TAKARAM OF THE THAN SAUCTEGARGACATTE 2281
                                                                                                                               DIED AWSK-ATTS TRIPPOPPER CANÇA PROCNSTISANCENSET SKAÇOD AGAGAT SOLAKAŞI DIDI
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHAPACTERISTICS:
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APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 14-MAY-1996
ATTOPNEY/AGENT INFORMATION:
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ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
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OPERATING SYSTEM (FOS
OPERAPE: FassSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                       TYPE, nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                         1461 base pairs
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Knowles, David
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                                                                                                                                                                           Conservative
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09-MAY-1997
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                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH, 5421 base
TYPE
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                                                                                                             TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
PEGISTEATICH INWBER 28,678
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE. Floppy disk
COMPUTER. IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS:DOS
SOFTWARE. Patentin Release #1.0, Version #1.25
CUFFENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ISOLA
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                                   FEATURE:
                                                                          HYPOTHETICAL: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE. Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  970 TTGGTCAATACTC-----TGTTTATGCCCGTGTGTCTCCAGAACACAAGGTTCGTATCG 917
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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LUCATION:
                NAME/KEY:
                                                       OPGANISM
                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER.
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                                                                                                                                                                                                                                                                      TELEPHONE. (212) 977-9550
TELEPAX: (212) 664-0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAGAAGAAGGTCGTCTGATATTTGATAACTTGAAGAAATCCATTGCTTACACCCTAACAA 2591
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                                                                                                                                                                                          5421 base pairs
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                                                       Homo Sapiens
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                                    US-08-338-579A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6068975
GENERAL INFORMATION:
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Query Match
                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
SEQUENTH: 5421 base pairs
TYPE: nucleic acid
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APPLICANT: Tanzi, Rudolph E.
TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S
TITLE OF INVENTION: DISEASE GENE
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                          HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                               NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGERENCE/DOCKET NUMBER: 05'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               MOLECULE TYPE:
                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/
FILING DATE: June 17, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                              NAME/KEY:
                                                                                                                       ORGANISM: Homo Sapiens
                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                       TOPOLOGY:
                                                            LOCATION:
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  1.6%; Score 57.2;
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  DB 3;
  Length 5421;
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                                                                                                               PCT-US94-09851-28
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                                            Query Match
Best Local Similarity 59.1%;
                                      Matches 117;
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INFORMATION FOR SEQ ID NO: 28:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REGISTATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: ISOLATION AND USES OF A WILSON'S TITLE OF INVENTION: DISEASE GENE
2292 CACGGAGATTGTCTTTGCTAGGACCTCTCCTCAACAGAAGCTCATCATTGTGGAGGGCTG 2351
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                                                                                                                                                                        FEATURE
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                       TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                     LOCATION:
                                                                                                                                                                                        ORGANISM:
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7: United States of America
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30 Rockefeller Plaza
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                                      Conservative
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                                                          1.6%; Score 57.2; DB 5; Length 5421; 59.1%; Pred. No. 6.3e-05;
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                                        0; Mismatches 78; Indels
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US-08-232-463-14/c
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                                                                                                                          Best Local Similarity 5.7%; Pred No. 0.0019; Matches 17; Conservative 160 Minner.
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEC ID NO. 14
SEQUENCE CHARACTER STICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_LOS
SOFTWARE: PatentIn Pelase #1 0, Version
CURRENT AFELICATION CATA.
APPLICATION NUMBER: US/08/232,463
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER 30
TELECOMMUNICATION INFORMATION
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: PECOMETNANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA
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ATTORNEY/AGENT INFORMATION.
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CLASSIFICATION.
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APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving The EPO and LLT Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SCETWARE: Patentia Felcase #1 5, Version #1
CUPPENT APPLICATION DATA
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ANDRESSEE: Curtis P. Ribando
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LOCATION:
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REGISTRATION NUMBER
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TOPOLOGY: lin
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US-09-461-697-462
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RESULT 14
US-09-041-886-18
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APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
FILE REFERENCE: 10001-005-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 462
LENGTH: 979
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CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
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                                                                                                                   190 CTAGTCTCCAGCCACAGGACCCGGGCGCGGGGCCCGCAGCGCCG 232
                                                                                                                                                             1.4%; Score 51.2; DB 1; Length 8438; Local Similarity 61.0%; Pred. No. 0.003; Les 83; Conservative 0; Mismatches 53; Indels 0
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                                                                              565 GCATGEGCECEGCECTGEEETTBGECETTGEEECETGTECEEG 607
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                                                                                                                                                                                                                                                                              10 GCGGGAGGAGGCGGACACGTGGCAGCGGCGGCAGCAGCAGCAGCAGCAGCAGCAGCA 69
                                                                                                                                                                                                                                                                                                                                                                                                                      Match 1.4%;
Local Similarity 54.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGAGCCTCGGCGGGAGGAGGCGGACACGTGGCAGCGGCGGCGGCAGCAGCAGCAGCAGCAGCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGCCCTAGTTCCCGC 136
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                                                                                                                                                                                                                                                                                                                                                                                                     122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 51; DB 4; Length 979; 
Pred. No. 0.0011; 
0; Mismatches 100; Indels
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                                                                                                                        US-08-118-200-1
                                                                                                                                         RESULT 15
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GENERAL INFORMATION:
APPLICANT: SUTHERLY
APPLICANT: RICHARDS
APPLICANT: SCHLESS:
APPLICANT: NAGARAJJ
                                                                                   Sequence 1, Application US/08118200 Patent No. 6197500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 30. Grandiego
                                                                                                                                                                                                                              211
                                                                                                                                                                                                                                                                                               151 GGCTCCACTCTCCCAGCCGGGAGCTGCTCTCTCTTCTAGTCTCCAGCCACAGGACA
                                                                                                                                                                                                                                                                                                                                                                                                          840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                     91 GCCGGCCGTCCTCCTCTTTCCTCCGGCGGCAGCCCTAGTTCCCCGCCTCTCGGCTCCCCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 1.3%; Score 49; DB 4; Length 4481; Local Similarity 51.6%; Pred. No. 0.0082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 4481 base pairs
                                                                                                                                                                                              CTCCTCGGTGGTCGCGGCGACCTCCGGCGGCGGGAGG 876
                                                                                                                                                                                                                              CGGCGCGGGCCCGCACCATGGGGAAGG 247
                                                                                                                                                                                                                                                               GCAGCCGCCGCCGCGCTGCCAATGTCCGCAAGCCGGCGGCAGCGGCCTTCTAGCGTC 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bredesen, Dale E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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 RICHARDS, Robert I
SCHLESSINGER, David
NAGARAJA, Ramaiah
                                                   SUTHERLAND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163..4099
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                                                   Grant
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Search completed: March 7, 2003, 00:26:32 Job time : 348 secs
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.25

CUERENT APPLICATION DATA:

APPLICATION NUMBER: US/08/118,200

FILING DATE: 09-SEP-1993

CLASSIFICATION: 435

PRIOP APPLICATION DATA:

PRIOP APPLICATION DATA:

PRIOP APPLICATION DATA:

PRIOP APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1028 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NIMBER: US 07/
FILING DATE: C4-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NIMBER: 020
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COPPESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION UNDEE: US 07/672,232
FILING DATE: 20-MAR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED TITLE OF INVENTION: FRAGILE X SYNDROME
                                                                                                                                                   504 CC 505
                                                                                                                124 CC 125
                                                                                                                                                                                                                                 STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Crane-Feury, Sharon E REGISTRATION NUMBER: 36,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                        4 GCCTCGGGGGGAGGAGGCGGACACGTGGCAGCGGCAGCAGCAGCAGCAGCAGCAGCGGCG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Virginia
TRY: United States
22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAKER, Elizabeth
MULLEY, John C
MANDEL, Jean-Louis
PRITCHARD, Melanie April
LYNCH, Michael
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KREMER, Eric J
                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                1.3%; Score 48.4; DB 4; Length 1028; 62.3%; Pred. No. 0.0056;
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                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                               Indels
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OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478924 seqs, 333959956 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-040-722-3
3636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ggagcctcggcgggaggagg.. . . . . agatggctattataacggaa 3636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   957848
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

| O | O | | | | | | | | | | | | | | | | | | | |
|--------------------|-------|----------------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|-------------------|-------------------|-------------------|------------------|------------------|------------------|-----------------|-----------------|-------------------|-------------------|-----------------|
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| 290.4 | 290.4 | | () () () | 330 | 343.2 | 367 | 432.6 | 432.6 | 432.6 | 432.6 | 486 | 486 | 750 4 | 779.8 | 780.2 | 844.4 | 870.8 | 1127.4 | 1320.4 | Score |
| 8.0 | α | 0 1 | درز | ý.1 | 9.4 | 10.1 | 11.9 | 11.9 | 11.9 | 11.9 | 13.4 | 13.4 | 20.6 | 21.4 | 21.5 | 23.2 | 23.9 | 31.0 | 36.3 | Match Length DB |
| 364 | 50 | | c, C, | 432 | 420 | 447 | 5 33 | 533 | 533 | 533 | 569 | 569 | 1355 | 1355 | 1355 | 1338 | 1338 | 3053 | 1338 | Length |
| æ | u | 0 | C | 10 | 10 | 9 | 12 | 10 | 10 | ω | 9 | 9 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | |
| NS-09-8/8-1/8-890 | | 116 - 10 - 046 - 935 - 890 | US-09-960-352-1493 | US-09-960-352-6292 | US-09-950-352-6966 | US-U9-796-697-6744 | US-10-00/-805-4/1 | US-09-339-338-271 | US-09-604-287A-271 | US-10-076-622-271 | US-09-878-178-809 | US-10-046-935-809 | US-09-870-472-10 | US-09-8/0-4/2-12 | US-09-870-472-11 | US-09-870-472-8 | US-09-870-472-9 | US-09-834-9/5-96/ | US-09-870-472-7 | |
| ochacises and sign | | Semience 890, App | Sequence 1493, Ap | Sequence save, Ap | Sequence over, me | <i>-</i> | | sequence 271 App | Sequence 2/1, App | | 3 0 | Sequence out, Apr | 0 10 0 | 1 , | 3 ; | | 0 4 | 0 0 | Sequence 7, Appli | PURCE FOR FORE |

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| 444 54 | 41 42 | 30 | (U (| 320 | 200 |
| 94.8 94 86.2 | 103.8 | 117.2 117.2 110.4 105.2 | 121.4 117.4 117.4 | 149.4 147 142 133.6 127.2 | 267 234.6 228.6 225.8 225.8 171.8 |
| 2.6 | 2.2.2. | 22333 | 3.23 2.23 | 3.9 3.7 3.5 | |
| 3063 181 968 | 3210 | 534 831 1939 3186 | 14286 1493 1493 | 797 190 2488 2676 13932 | 415 468 768 269 3053 26668 215 |
| 10 | 10 | 10 | 10 9 | 10 10 9 | 10 10 10 10 10 |
| US-09-833-381-505 US-09-833-381-641 | US-09-070-927A-374 US-09-070-927A-374 | US-09-974-300-6433 US-09-974-300-6381 US-09-822-830A-406 US-09-938-842A-1957 US-09-960-352-10862 | US-09-070-927A-162 US-09-925-299-180 US-09-925-299-180 | US-09-834-975-299 US-09-864-761-22127 US-09-974-300-2016 US-09-738-626-1708 US-09-070-927A-363 | US-09-960-252-6766 US-09-864-761-6168 US-09-810-943-3 US-09-810-943-3 US-09-864-761-21979 US-09-834-975-967 US-09-834-975-485 US-09-834-975-485 US-09-834-975-485 |
| Sequence 1505, Ap Sequence 641, App | Sequence 1594, Ap Sequence 374, App Seguence 2553, Ap | Sequence 0433, Ap Sequence 6381, Ap Sequence 406, App Sequence 1957, Ap Sequence 10862, A | Sequence 180, App Sequence 180, App Sequence 180, App | Sequence 22127, Ap Sequence 2016, Ap Sequence 1708, Ap Sequence 363, App Sequence 363, App | Sequence 6766, Ap Sequence 6168, Ap Sequence 33, Appl Sequence 21979, A Sequence 967, App Sequence 222, App Sequence 485, App Sequence 485, App |

ALIGNMENTS

RESULT 1

| and uses 0; |
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 967
LENGTH: 3053
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Best Local Similarity
Matches 1341; Conserv
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, P
TITLE OF INVENTION: OF HUMAN CANCERS
FILE REFERENCE: MRI-016B
CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR APPLICATION NUMBER: 60/197,538
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-870-472-9

Sequence 9, Application US/09870472 Fatent No. US20020095023A1

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APPLICANT: LEE, Kyunglim et al.

TITLE OF INVENTION: IgE-dependent histamine-releasing factor(HRF) receptor, HRF-
TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 1599-0198P
CURRENT APPLICATION NUMBER: US/09/870,472
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: KR10-2000-0030130
PRIOR APPLICATION NUMBER: KR10-2000-0030130
PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: KOPATIN 1.71

SEQ ID NO 9
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                                  TTCCAGTTTGACACTGATGAAGTCAATTTCCCCGTGGATAACCTCTGCTTCGTGGGTCTT 2001
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  TTTGCCTTTGACTGATGACGTGAACTTCACCACAGACAACCTTTGCTTCGTGGGTCTC
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                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT. LEE, Kyunglim et al.
APPLICANT. LEE, Kyunglim et al.
TITLE OF INVENTION: IgE-dependent histamine-releasing factor(HRF) receptor, HRF-
TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 1599-0198F
CURPENT APPLICATION NUMBER: US/09/870,472
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: KR10-2000-0030130
PRIOR TOTAL 2003 06 01
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                        SEQ ID NO 8
LENGTH: 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/09870472 Patent No. US20020095023A1
                                       Best Local Similarity Matches 1028; Conserv
                                                                           Query Match
                                                                                                                                                                                                                                                                                                  SOFTWARE: KOPATIN 1.71
                                                                                                                             FEATURE:
NAME/FEY. CASURE
LOCATION: (1) ...(1338)
COTHER INFORMATION: n = a,c,g,t, any unknown or other
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                                                                                                                                                                                                                                            TYPE: DNA
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                                                                            GACTTGAAGGACATGACCTCTGAGGAGCTGGATGACATTTTGCGGTACCACACGGAGATT 2301
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Patent No. US20020095023A1
GENERAL INFORMATION:
APPLICANT: LEE, Kyunglim et al.
APPLICANT: LEE, Kyunglim et al.
TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and uses
TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and uses
TITLE OF INVENTION: thereof
FILE PERPENCE: 1599-0198P
CURRENT APPLICATION NUMBER: US/09/870,472
CURRENT FILING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: KOPATIN 1.71
SEQ ID NO 11
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Local Similarity 75.7%;
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RESULT 6 US-09-970-472-12 ; Sequence 12, Application US/09870472 ; Patent No. US20020095023A1

GAGGGCCNNGCCTGATCTTTGACAACTTGAAGAAA 1355

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APPLICANT. LEE, Kyundin et al.
APPLICANT. LEE, Kyundin et al.
TITLE OF INVENTION: IGE-dependent histamine-releasing factor(HPF) receptor, HRF-
TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and uses
TITLE OF INVENTION: thereof
FILE REFERENCE: 1590-0198F
CURRENT APPLICATION NUMBER: US/09/870,472
CURRENT APPLICATION NUMBER: US/09/870,472
CURRENT FILING IATE. 200-06-01
PRIOR APPLICATION NUMBER: KP10-2000-0030130
PRIOR APPLICATION NUMBER: KP10-2000-0030130
PRIOR FILING DATE. 2009-06-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: KCFATIN 1.71
SEQ ID NO 12
FEATURE:
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OTHER INFORMATION: n - a,c,g,t, any unknown or other
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GENERAL INFORMATION:
APPLICANT: LEE, Kyunglim et al.
APPLICANT: LEE, Kyunglim et al.
TITLE OF INVENTION: TgE-dependent histamine-releasing factor (HPF) receptor, HRF
TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and use
TITLE OF INVENTION: binding peptides, nucleic acids encoding the same, and use
TITLE REFERENCE: 1599-0198P
CURRENT FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2000-06-01
PRIOR FILING

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Sequence 10, Application US/09870472 Patent No. US20020095023A1

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; Sequence 809, Application US/10046935 ; Patent No. US20020156011A1 ; GENERAL INFORMATION:

RESULT 8 US-10-046-935-809

US-09-878-178-809

Sequence 809, Application US/09878178
Patent No. US20020177552A1
GENERAL INFORMATION:

APPLICANT: Jiang,

Yugiu

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CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 809
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Best Local
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
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LOCATION: 525
OTHER INFORMATION: n = A,T,C or G
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                                                                            AGAAAACTCATCATCAGGCGACGCCCTGGCGGCTGGGTGGAGAANGAAACCTACTATTAG
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                       CCCACTGCCCTGCACGCCGTGGAACAT 3336
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Secrist, Heather
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91.0%;
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Pred. No. 6.3e-117;
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US-10-076-622-271
Sequence 271, Application US/10076622
Publication No. US20030023036A1
GENERAL INFORMATION
APPLICANT: Houshon, Baymond L.
APPLICANT: Sleath, Faul P
APPLICANT: Persing, David H
TITLE OF INVENTIAL TEMPOSITION AND METHORS F-9
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APPLICANT. 3ecrist, Heather
TITLE OF INVENTION. *CAMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION. AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE. 210121.527
CURRENT FILING DATE. 2001 96-08
CURRENT FILING DATE. 2001 96-08
NUMBER OF SEQ ID NOS: 2237
SOFTMARE: FasuSEQ for Windows Version 4.0
SEQ ID NO 809
SEQ ID NO 809
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Best Local
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NAME/KEV: misc feature
LOCATION: (1)...(569)

OTHER INFORMATION: n = A,T,C or
-09-878-178-809
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TYPE, DNA
OPGANICM Homo sapien
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                                                                                                                                                                      CCCCCCCTCCTGCACGCCGTGGAACAT 3326
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Fred. No. 6.3e-117
0; Mismatches 51
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51; Indels
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OTHER INFORMATION: n = A,T,C or G
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CUMPENT AFFLICATION NUMBER: US/10/076,622
CUMPER OF FILING DATE: 2002-02-13
EUMPER OF SEQ In MOS. 627
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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NAME/KEY: misc_feature
.ccarion. 100, 137, 38
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TYPE: DNA
OPGANISM: Homo sapiens
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481 CATCGGAGCCCCAACACCTGTTGGTGATGAAGGGCCCCAGAAAGGAATCCT
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                                                                                                                                                                                                                   <u>AAAACCTACCTATTCTTAAGCGGGGCAGTTGCAGGAGATGCCTCTGAGTCAGCACTCTTAA</u>
                                                                                                                                                                                                                                        AAAACCIGCCTATCCTTAAGCSTGCAGIAGCGGGGAGACTGCTGAGGCGCTCTTAA 1669
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US-09-604-287A-271
US-09-604-287A-271
Sequence 271, Application US/09604287A
Fatent No. US20020064872A1
Fatent No. US20020064872A1
Fatent No. US20020064872A1
Fatent No. US20020064872A1
FAPPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE PEFERENCE: 210121.470C7
CUMPBENT APPLICATION UNMERS: US/09/604,287A
CUMPENT APPLICATION UNMERS: US/09/604,287A
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 271, Application US/09339338A Fatent No. US20020102602A1 GENERAL INFORMATION:
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US-09-339-338-271
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 271
LENGTH: 533
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                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEC ID NO 271 LENGTH: 533
                                                                                                                     APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C2
CURRENT APPLICATION UMBER: US/09/339,338A
CURRENT APPLICATION UMBER: US/09/339,338A
CURRENT OF SEQ. ID NOS: 315

NUMBER OF SEQ. ID NOS: 315
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LOCATION: (1) (533)
OTHER INFORMATION: n=A,T,C or G
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ORGANISM: Homo sapiens
                           TYPE: DNA
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Local Similarity 88.0%;
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; GENERAL INFORMATION
                                                                               US-10-007-805-271
                                                                                                       RESULT 13
                          Sequence 271, Application US/10007805 Patent No. US20020150581A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 468; Conservative
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LOCATION: (1)...(533)
OTHER INFORMATION: n=A,T,C or G
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                                                                                                                                                                               CATCGGAGCCCAACACCTGTTGGTGATGAAGGGCGCCCCAGAAAGGATCCT 532
                                                                                                                                                                                                                                                                                  TCGAGATACCCTTCAACTCCACCAACAAGAACCAGTTGTCTATTCATAAGAACCCCAACA 480
                                                                                                                                                                                                                                                                                                                                    TGGAGATTCCCTTCAACTCCACCAACAAGTACCAGCTCTCCATTCACAAGAACCCCAAACG 1729
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SOFTWARE: FASTSEC for Windows Version 4 0
SEQ ID NO 271
LENGTH: 533
TYPE: DNA
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APPLICANT: Vedvick, Thomas S.
APPLICANT: McNeill, Patricia D.
APPLICANT: Durham, Margarita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
                                                                                               FILE REFERENCE: 210121.470C10
CURRENT APPLICATION NUMBER: US/10/007,805
CURRENT FILING DATE: 2001-12-07
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                                                                            NUMBER OF SEQ ID NOS:
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Mitcham, Jennifer L.
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US-09-796-692-8244
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CURPENT APPLICATION NUMBER: US/09/746,602
CURPENT STITMS DATE 2001 33 01
PRIOR APPLICATION NUMBER: 60/196,126
PRIOR PRILING DATE 2000 03 01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR PILLNG DATE: 2000 04 28
PRIOR APPLICATION NUMBER: 60/200,770
PRIOR APPLICATION NUMBER: 60/200,770
PRIOR APPLICATION NUMBER: 60/200,770
PRIOR FILLNG DATE: 2000 04 28
PRIOR APPLICATION NUMBER: 60/200,770
PRIOR FILLNG DATE: 2000 05 01
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Publication No. US20020198362A1
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                                                                                                                                                                                                                                                                                                        APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE : TIMENTION - TOMPOSITIONS AND METHEOS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE : INVENTION: HEMATOLOGICAL MALIGNANCIES
EILE REPERENCE: 2077 001000
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88.0%, Fied. No. 5.3e 133;
varive 0; Mismatches 64, Indels
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PRIOR FILING DATE: 2000-05-04
PRIOR PELICATION NUMBER: 60/206,201
PRIOR PELICATION NUMBER: 60/206,201
PRIOR PELICATION NUMBER: 60/218,950
PRIOR PELICATION NUMBER: 60/218,950
PRIOR PELING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR APPLICATION NUMBER: 60/233,416
PRIOR PELING DATE: 2000-08-04
PRIOR PELING DATE: 2000-08-04
PRIOR PELING DATE: 2000-08-07
NUMBER: 0F SEQ ID NOS: 9597
NUMBER: 0F SEQ ID NOS: 9597
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Best Local Similarity
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                           TGGAGATTCCCTTCAACTCCACCAACA 1696
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TCGAGATACCCTTCAACTCCACCAACA 447
                                                                                   AGTGCATCGAGGTCTGCTGTGGCTCCGTGATJGAGATGAGAGAGAAGTACACCAAGATAG 1669
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Sequence F966, Application US/09060352
Patent No. US2000137139A1
GEMERAL INFORMATION
APPLICANT: Marron, Wesley C
APPLICANT: Marron, Wesley C
APPLICANT: Byatt, John C.
APPLICANT: Matchialagan, Nagappan
TITLE of INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LATATION AND
FILE REPERENCE: 16511.006/37-21(10298)C
CUPPENT APPLICATION NUMBER: US/09/960,352
CUPPENT FILING DATE: 2001.09-24
RUMBER CF SEQ ID NO 6966
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US-09-960-352 6966

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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION OLONG ID 10-LIB1058-001-Q1-K1-H9
US-09-960-352-6966
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Search completed: March 7, 2003, 02:59:13 Job time: 287 secs
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2020000000
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    March 6, 2003, 18:39:51; Search time 4780 Seconds (without alignments) 12319.412 Million cell updates/sec
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gb_est3:*

gb_est5:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| BQ900623 AGENCOURT | BQ900623 | 14 | 916 | 21.1 | 767.4 | 0 |
|--------------------|----------|----|-----------------|--------|--------|--------|
| BQ891199 AGENCOURT | BQ891199 | 14 | 907 | 21.2 | 769.8 | 5 |
| BQ715991 AGENCOURT | BQ715991 | 14 | 935 | 21.6 | 786.8 | 4 |
| BC023175 Mus muscu | BC023175 | 11 | 1009 | 25.0 | 910.B | ų. |
| BC031389 Mus muscu | BC031389 | 11 | 1131 | 28.3 | 1027.8 | tJ |
| BC013763 Homo sapi | BC013763 | 11 | 3846 | 52.0 | 1889.2 | 1 |
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| 9696696 969666 969666 | 917501 AGENCOUR 519260 E0324089 559260 E0324089 98370 EST250073 | 9259 6025/750 60875 AGENCOUR 6063 60328471 7098 60323866 9235 603240866 9236 UI-R-DNI | 47185 72175 55880 92097 85304 67781 | 003 603 874 876 881 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 | 1904878 60316890 1407185 60291909 2931254 AGENCOUP Q943860 AGENCOUP 1102401 60288807 Q714959 AGENCOUP M915431 AGENCOUP M915431 AGENCOUP |

ALIGNMENTS

| | PEMAPK COMMENT | CORNAL | AUTHORS TITLE | REFERENCE | KEYWORDS SOURCE ORGANISM | RESULT 1 BC013763 LOCUS DEFINITION ACCESSION VERSION |
|---|---|---|---|---|---------------------------------------|---|
| Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalon@bcm.tmc.edu. | NIH-MGC Project UPL: http://mgc.nci nih gov Contact: MGC help desk | Submitted (04-58-2001) National Institutes of health, Mammatian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA | Strausberg,R. Direct Submission O'Derect Submission O'Derect Submission | <pre>Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3846)</pre> | HTC. Homo sapiens. Homo sapiens | BC013763 BC013763 3846 bp mRNA linear HTC 07-SEP-2001 HCmo sapiens, clone IMAGE:3874001, mRNA. BC013763.1 GI:15489327 |

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BASE COUNT
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Matches 2307; Conservative
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    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 13 Row: n Column: 9
This clone has the following problem: incomplete processing.
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/clone_lib="NHH MGC_67"
/lab_hcst-"DH10E"
/note="Vector: pCMV-SPORT6"
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ATCACAGCAAAGCGATTGCTAAAGGGGGTGGGGATATATCTCAGAAGGGTAACGAGACGGTG 2140
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2161 GAAGACATTGCTGCCCGCCTCAACATTCCAGTGAACCAGGTGAACCCCCAGAGATGCCAAG 2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACGGGCAGCAGTGGACCTACGAGCAGAGGAAGATTGTGGAGTTCACCTGCCACACGGCC 3000
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                                                                                                                                                                                                                                                                                                                                 AACTCGGTCTTCCAGCAGGAGGACATGAAGAAGATCCTGATCTTCGGGCTGTTTGAGGAG 2990
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TITLE
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  2646 CACCGTGACCATCCTCTGCATTGACTTGGGCACTGACATGGTTCCCGCCATCTCTCTGGC
                                                                                                                                                                                                              2526 AGAAGGTCGTCTGATATTTGATAACTTGAAGAAATCCATTGCTTACACCCTAACAAGTAA 2585
                                                       61 CATTCCGGAAATCACCCCCTTCTTGATATTTATTATTGCAAACATTCCACTGCCCCTGGG 120
                                                                                                                                                             μ
                                                                                        CATTCCGGAAATCACCCCCTTCTTGATATTTATTGCAAACATTCCACTGCCCCTGGG
                                                                                                                                                          AGAAGGTCGTCTGATTTTTGATAACTTGAAGAAATCCATCGCTTACACCCTAACCAGTAA 60
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Mus musculus, clone IMAGE:4946041,
BC031389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I M.A.G E Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 60 Row: c Column: 1
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Li, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.B., Lawrence, S., Martin, P.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation. Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (96-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email cgapbs-r@mail.nih gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project UPL: http://mgc.nci.nih gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC031389.1 GI:21595237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                               181
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                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Mammary tumor C3(1)-Tag model. Infiltrating
ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
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                                                                                                                                                                                                                                                                                         Score 1027 8; DP 11; Length 1131; Pred. No. 1.9e-261;
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                                                                                                                                          GCCTTTTTGTTTTTGTAAAAAAGGAAAACCTGGAAAGACTGAAAGATTACGTTTTATATC
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                                  GCATCCGAGAGACCTGGGATGACCGCTGGATTAATGATGTGGAGGACAGCTACGGGCAGC
GCATCCGAGAGACCTGGGATGÁCCGCTGGGTCAACGATGTGGAGGACAGCTACGGGCAGC 300
                                                                                                  GCTTCTTCACTTACTTTGTGATTCTGGCTGAGAACGGTTTCCTGCCCTTTCACCTGTTGG
                                                                                                                                  GCTTCTCACTTATTTTGTGATTCTTGGCTGAGAACGGTTTTCCTTGCCCCTTTCACCTGTTGG 2890
                                                                                                                                                                                                                                                    TGAACGAGCGTCTGATCAGCATGGCCTATGGACAGATCGGTATGATCCAGGCCCTGGGAG 2830
                                                                                                                                                                                                                                                                                                   AGCAAGCTGAGAGCGACATCATGAAGAGGCAGCCCAGAAACCCCCAAAACCGGACAAACTTG
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project UPL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (04-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Pages 11A07, Bethosda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1_to 1009)
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Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone has the following problem:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Mammary tumor. C3(1)-Tag mode ductal carcinoma. 5 month old virgin mouse. /clone_libe="NCI CGAP_Mam6" /lab_host="DH10B" /note="Vector: pcMv-SPORT6" a 247 c 276 g 236 t
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/db_xref="taxon:10090"
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                Tissue Procurement: Susan L. Sullivan, PhD.

cDNA Library Preparation: ResGen, Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                    NIH-MGC http://mgc nci nih.gov/
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                      National Institutes of Health, Mammalian Gene Unpublished (1999)
found through the I.M.A.G.E. Consortium/LLNL at:
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/clone lib="WIH MGC 129"
/lab_host="DH108 (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally, Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this a NIH MGC Library."
a 240 c 251 g 216 t 1 others
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High quality sequence stop: 590.
Location/Qualifiers
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Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L.
Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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REFERENCE COMMENT JOURNAL TITLE AUTHOPS Eukaryota, Matazoa, Chordata, Cianiata, Vert-hrata, Eur-lo-stomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus 1 (bases 1 to 916)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Pobert Strausherg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Progurement: Susan L

cDNA Library Preparation: ResGen,

sullivan,

Invitrogen Corp

KEYWORDS SOUPCE ACCESSION VERSION

ORGANISM

Mus musculus ສະເພພ ສຣກພິບ DEFINITION

916 b AGENCOURT 8758360 NIH_MGC_120 5', mRNA Sequence. 82000623 RQ000623.1 GI:22292644

916 kp mkka I 129 Mus musculus

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FEATURES
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                                                                                                                                                                                                                                                                     GAGATTGTCTTTGCTAGGACCTCTCCTCAACAGAAGCTCATCATTGTGGAGGGCTGCCAG 2355
                                                                                                                                                                                                                                                                                                                                                                                         GGCAGTGACTTGAAGGACATGACCTCTGAGGAGCTGGATGACATTTTGCGGTACCACACG 2295
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/clone lib="NIH MGC 129"
/lab_host="DH10B (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH MGC Library."
a 252 c 243 g 211 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI904878 895 bp mRNA linear EST 16-OCT-2001
603168903F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5256937 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 893.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://image.llnl.gov
Plate: LLAM11649 row: e column: 02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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                                                                                      Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
3 237 c 245 g 292 t
                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5256937"
/clone=11b="NCI CGAP_LU33"
/tissue_type="pooled lung tumors"
/lab_host="DH10B (phage-resistant)"
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20.7%;
94.0%;
  Score 753.6, DB 13
Fred. No. 1.2e-188,
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                                                                                                                                                                                                    TGGACCGATGCAGTTC 1796
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Mus musculus
Eukaryita, Metazca, Cherdata, Craniata, Vertebiata, I
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae,
                                                                                                     859 bp FRNA linear EST 14-AUG-2001
602010002F1 NCI_CGAP_Lu3 Mus musculus CENA Clone IMAGE:5055814 57,
                                                                                BI407185
                                                                                           mRNA sequence.
                                                                    BI407185.1 GI:15168108
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      Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                 74
                                                     GTAGTGCAGTGGGCTGACTTGGTCATCTGCAAGACCAGAAGGAATTCTGTCTTCCAGCAG 3078
                                                                                                                                                                                                                                                                                                                                            CGTCTGATCAGCATGGCCTATGGACAGATCGGTATGATCCAGGCCCTGGGAGGCTTCTTC 2838
                                                                                                                                                                                                                                                                      ACTIAITITGIGATTCIGGCIGAGAACGGITTCCTGCCCITTCACCTSITGGGCATCCGA 2898
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                                                                                                                                                TACSAGCAGAGGAAGATTGTGGAGTTCACCTGCCACACGGCCTTCTTTGTCAGTATCGTG 3018
                                                                                                                                                                                                   GAGACCTGGGATGACCGCTGGGTCAACGATGTGGAGGACAGCTACGGGCAGCAGTGGACC 313
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                                                                                                                                TÁCGAGCÁGAGGAAGATCGTGGAGTTCACCTGCCATACAGCGTTCTTTGTCAGTATTGTG 373
                                                                                                                                                                                                                               GAGACCTGGGATGACCGCTGGATTAATGATGTGGAGGACAGCTACGGGGAGGTAGTGGATG
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Place LLAM11151 row: h column: 23
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Contact Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procutement Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 858)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gen-
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Location/Qualifiers
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/db_xref="taxon:10090"
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                         Query Match 20.7%;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A G E. Consortium/LLNL at
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM13888 row: n column: 05
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1 (bases 1 to 947)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: The Cepko Laboratory
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AGENCOURT_8926939 NCI_CGAP_Cc24 Mus
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                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 607.
Location/Qualifiers
     Conservative
                                                                                                              /clone_lib="NCI_CGAP_Co24"
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/note="0rgan: colon; Vector: pCMV-SpORT6; Site_1: NotI;
/note="0rgan: colon; Vector: pcmv-spoRT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
a 254 c 262 g 216 t 10 others
                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:6394948"
                                                                                                                                                                                                                                                                                                                                      /strain="FVB/N"
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  0; Mismatches
                      Score 751.8; DB 14
Pred. No. 3.7e-188;
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RESULT 10 BQ943860

DEFINITION
ACCESSION
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BQ943860 BQ943860.1 GI:22359338 EST.

917 bp mRNA linear EST AGENCOURT 8801902 NCI CGAP Mam2 Mus musculus cDNA clone IMAGE:6439036 5', mRNA sequence.

KEYWORDS

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                                                GGGCTGCCCGAAAAACACCGTGGACGGGGACGACAGCGGG 3525
                                                                                                      ATGCAGACGTCCTGGATGAAACAGTANCTGTAACGGGGGGGGGNNNNNNGGGGGGGGAGA
                                                                                                                                                    ATCCAGACGTCCTGGAATGAAGCATGTAGCTGTAATGGGG------GGCGGGGGGGA 3485
                                                                                                                                                                                                          ACTTCAAGTCTTGGAGCTCGNGACTCTACCCCTGGGTAGAAGCACCAAGCATGGGGNGGG
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                                                                                                                   AAGCGCATGGCGAGGAAGAACTGCCTGGTGAAGAACTTGGAAGCTGTGGAGACCTTGGGG
                                                                                                                                                    ANGUGATGGGAGGANGAACTGCCTGGTGAAGAACCTGGAAGCTGTGGAGACCTTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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NIH-M3C http://mgc.nci_nih.gov/
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251 2 245 g 202 t 1 others
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/tissue_type="tumor,_biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
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/clone="IMAGE:6439036"
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    Mismatches

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Pred. No. 3.8e-186;
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                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 883)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Plate: LLAM11118 row: b column:
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/db_xref="taxon:10090"
/clone="IMAGE:5042994"
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/clone="IMAGE:5042994"
/lab_host="DH10B" (TI_phage-resistant)"
/note="Organ: kidney: Vector: pcmV SPOPT6; Site_1: NotI;
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Site_2: Sall, Cloned unidatestionally Primer: Cligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies, Note: this is a NcI_CSAP Library | "
a 219 c 246 g 207 t
                                                                                                                                                                                              strain="FVB/N"
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Best Local Similarity 93.4%;
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                                                                                                                                                                                                                  TGGTCATCTGCAAGACCAGAAGGAATTCTGTCTTCCAG 3075
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                                                                                                                                                                                                                                                                                                       TGGAGTTCACCTGCCACACGGCCTTCTTTGTCAGTATCGTGGTAGTGCAGTGGGCTGACT 3037
                                                                                                                                                                                                                                                                                                                                                              GGGTCAACGATGTGGAGGACAG-TACGGGCAGCAGCTGGACCTACGAGCAGAGGAAGATCG 778
5', mRNA sequence.
BQ714959
BQ714959.1 GI:21853858
                                                       BQ714959 954 bp mRNA linear EST 16-JUL-2002
AGENCOURT 8482883 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6306076
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Pred. No. 5.4e-186;
0; Mismatches 54;
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cDNA Library Preparation: ResGen, Invitrogen Corp cDNA Library Arrayed by The I M A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13721 row: g column: 05
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Tissue Procurement: Susan L. Sullivan, PhD.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone=!b="NIH MCC 129"
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/note="Organ: olfactory epithelium; Vector:
pcMV-SPORT6.1.cdb; Site_1: EcoRV; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: th is a NIH MGC Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-remail_nih_gov
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                                                                       GAACATTGCCTTCTTTCAACCAATTGTGTTGAAGGCACCGCACGTGGTATTGTTGTCTA 303
                                                                                                 GAACATTGCCTTCTTCTCAACCAACTGTGTTGAAGGAACTGCACGTGGCATCGTTGTGTA 1016
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cDNA Library Arrayed by: The I.M.A.G.E. (Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution. MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2533 row: d column: 24
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Location/Qualifiers
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_most="DH10B (phage-resistant)"
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insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
4 others
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                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                      Plate: LLCM1967 row: a column: High quality sequence stop: 726.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EcoRI; cola made by oligo-dT prining. Directionally cloned into EcoRI/MhoI sites using the following 5' adaptor ggcAcGAG4G | Library constructed by Ling Hong in the laboratory of forald M. Putin "Interstry of "alifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript I FT (Life Technologies) Note: this is a NIH MGC Library."
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